GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 20, 2005, 07:26:03 ; Search time 62 Seconds
(without alignments)
67.337 Million cell updates/sec

Title: US-10-668-181-6
Perfect score: 63
Sequence: 1 CWINNNAVFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	63	100.0	10	18	US-10-668-181-6	Sequence 6, Appli
2	63	100.0	513	9	US-09-818-264-4	Sequence 4, Appli
3	63	100.0	513	16	US-10-473-339-4	Sequence 4, Appli
4	63	100.0	936	15	US-10-295-027-490	Sequence 490, App
5	63	100.0	936	15	US-10-173-999-18	Sequence 18, Appl
6	63	100.0	967	15	US-10-295-027-488	Sequence 488, App
7	63	100.0	967	15	US-10-173-999-16	Sequence 16, Appl
8	63	100.0	993	15	US-10-173-999-14	Sequence 14, Appl
9	63	100.0	1000	15	US-10-295-027-486	Sequence 486, App
10	63	100.0	1000	15	US-10-173-999-22	Sequence 22, Appl
11	63	100.0	1014	14	US-10-054-044A-4	Sequence 4, Appli
12	63	100.0	1014	14	US-10-120-604-4	Sequence 4, Appli
13	63	100.0	1014	14	US-10-120-604-139	Sequence 139, App
14	63	100.0	1014	14	US-10-225-567A-428	Sequence 428, App
15	63	100.0	1014	15	US-10-295-027-492	Sequence 492, App
16	63	100.0	1014	15	US-10-295-027-810	Sequence 810, App
17	63	100.0	1014	15	US-10-295-027-847	Sequence 847, App
18	63	100.0	1014	15	US-10-173-999-20	Sequence 20, Appl
19	63	100.0	1014	16	US-10-741-657A-2	Sequence 2, Appli
20	63	100.0	1014	16	US-10-723-860-2455	Sequence 2455, Ap
21	63	100.0	1014	16	US-10-349-528-24	Sequence 24, Appl
22	63	100.0	1014	20	US-11-070-456-4	Sequence 4, Appli
23	63	100.0	1014	20	US-11-070-456-139	Sequence 139, App
24	63	100.0	1038	18	US-10-668-181-2	Sequence 2, Appli
25	63	100.0	1252	17	US-10-505-486-38	Sequence 38, Appl
26	54	85.7	717	14	US-10-054-044A-2	Sequence 2, Appli
27	44	69.8	238	18	US-10-500-240-92	Sequence 92, Appl
28	44	69.8	252	18	US-10-500-240-94	Sequence 94, Appl
29	44	69.8	277	18	US-10-500-240-87	Sequence 87, Appl
30	44	69.8	284	18	US-10-500-240-88	Sequence 88, Appl
31	44	69.8	284	18	US-10-500-240-90	Sequence 90, Appl
32	43	68.3	94	16	US-10-425-115-209272	Sequence 209272,
33	43	68.3	662	13	US-10-036-328A-8	Sequence 8, Appli
34	43	68.3	714	9	US-09-818-264-2	Sequence 2, Appli
35	43	68.3	714	16	US-10-473-339-2	Sequence 2, Appli
36	43	68.3	733	13	US-10-036-328A-4	Sequence 4, Appli
37	43	68.3	1138	13	US-10-036-328A-6	Sequence 6, Appli
38	43	68.3	1210	13	US-10-036-328A-2	Sequence 2, Appli
39	41	65.1	42	14	US-10-097-065-236	Sequence 236, App
40	41	65.1	42	15	US-10-372-876-236	Sequence 236, App
41	40	63.5	48	15	US-10-424-599-220247	Sequence 220247,
42	40	63.5	99	15	US-10-424-599-279922	Sequence 279922,
43	40	63.5	104	15	US-10-424-599-211553	Sequence 211553,
44	40	63.5	390	14	US-10-081-816-39	Sequence 39, Appl
45	40	63.5	390	15	US-10-447-328-58	Sequence 58, Appl

ALIGNMENTS

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RESULT 1
US-10-668-181-6
; Sequence 6, Application US/10668181
; Publication No. US20050202439A1
;   GENERAL INFORMATION:
;        APPLICANT: OSTERHOFF, CAROLINE
;                   IVELL, RICHARD
;        TITLE OF INVENTION: EPIDIDYMIS-SPECIFIC RECEPTOR PROTEIN
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22201
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/668,181
;             FILING DATE: 24-Sep-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/041,745
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B.J.
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 35-125
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 703-816-4000
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;            TELEFAX: 703-816-4100
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-668-181-6

  Query Match          100.0%;  Score 63;  DB 18;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0018;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 CWINNNAVFY 10


RESULT 2
US-09-818-264-4
; Sequence 4, Application US/09818264
; Patent No. US20020142951A1
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al.
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL001193
;  CURRENT APPLICATION NUMBER: US/09/818,264
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 513
;   TYPE: PRT
;   ORGANISM: Human
US-09-818-264-4

  Query Match          100.0%;  Score 63;  DB 9;  Length 513;
  Best Local Similarity   100.0%;  Pred. No. 0.072;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        379 CWINNNAVFY 388


RESULT 3
US-10-473-339-4
; Sequence 4, Application US/10473339
; Publication No. US20040171540A1
; GENERAL INFORMATION:
;  APPLICANT: PE CORPORATION (NY)
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL001193
;  CURRENT APPLICATION NUMBER: US/10/473,339
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: PCT/US02/09317
;  PRIOR FILING DATE: 2002-03-27
;  PRIOR APPLICATION NUMBER: 09/818,264
;  PRIOR FILING DATE: 2001-03-28
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 513
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-473-339-4

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Db        379 CWINNNAVFY 388


RESULT 4
US-10-295-027-490
; Sequence 490, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 490
;   LENGTH: 936
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-490

  Query Match          100.0%;  Score 63;  DB 15;  Length 936;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
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Db        748 CWINNNAVFY 757


RESULT 5
US-10-173-999-18
; Sequence 18, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
;  APPLICANT: Mack, David H.
;  APPLICANT:  Gish, Kurt C.
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;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
;  TITLE OF INVENTION:  and Methods of Screening for Modulators of Ovarian
;  TITLE OF INVENTION:  Cancer
;  FILE REFERENCE: 018501-002420US
;  CURRENT APPLICATION NUMBER: US/10/173,999
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: US 60/299,234
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/315,287
;  PRIOR FILING DATE: 2001-08-27
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/372,246
;  PRIOR FILING DATE: 2001-04-12
;  NUMBER OF SEQ ID NOS: 163
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 936
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-173-999-18

  Query Match             100.0%;  Score 63;  DB 15;  Length 936;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
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Db        748 CWINNNAVFY 757


RESULT 6
US-10-295-027-488
; Sequence 488, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 488
;   LENGTH: 967
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-488

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  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
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Db        728 CWINNNAVFY 737


RESULT 7
US-10-173-999-16
; Sequence 16, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
;  APPLICANT: Mack, David H.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
;  TITLE OF INVENTION:  and Methods of Screening for Modulators of Ovarian
;  TITLE OF INVENTION:  Cancer
;  FILE REFERENCE: 018501-002420US
;  CURRENT APPLICATION NUMBER: US/10/173,999
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: US 60/299,234
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/315,287
;  PRIOR FILING DATE: 2001-08-27
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/372,246
;  PRIOR FILING DATE: 2001-04-12
;  NUMBER OF SEQ ID NOS: 163
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 967
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-173-999-16

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Qy          1 CWINNNAVFY 10
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Db        728 CWINNNAVFY 737


RESULT 8
US-10-173-999-14
; Sequence 14, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
;  APPLICANT: Mack, David H.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
;  TITLE OF INVENTION:  and Methods of Screening for Modulators of Ovarian
;  TITLE OF INVENTION:  Cancer
;  FILE REFERENCE: 018501-002420US
;  CURRENT APPLICATION NUMBER: US/10/173,999
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: US 60/299,234
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/315,287
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;  PRIOR FILING DATE: 2001-08-27
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/372,246
;  PRIOR FILING DATE: 2001-04-12
;  NUMBER OF SEQ ID NOS: 163
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; SEQ ID NO 14
;   LENGTH: 993
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-173-999-14

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
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Db        754 CWINNNAVFY 763


RESULT 9
US-10-295-027-486
; Sequence 486, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 486
;   LENGTH: 1000
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-486

  Query Match            100.0%;  Score 63;  DB 15;  Length 1000;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
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Db        761 CWINNNAVFY 770


RESULT 10
US-10-173-999-22
; Sequence 22, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
;  APPLICANT: Mack, David H.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
;  TITLE OF INVENTION:  and Methods of Screening for Modulators of Ovarian
;  TITLE OF INVENTION:  Cancer
;  FILE REFERENCE: 018501-002420US
;  CURRENT APPLICATION NUMBER: US/10/173,999
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: US 60/299,234
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/315,287
;  PRIOR FILING DATE: 2001-08-27
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/372,246
;  PRIOR FILING DATE: 2001-04-12
;  NUMBER OF SEQ ID NOS: 163
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 1000
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-173-999-22

  Query Match            100.0%;  Score 63;  DB 15;  Length 1000;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        761 CWINNNAVFY 770


RESULT 11
US-10-054-044A-4
; Sequence 4, Application US/10054044A
; Publication No. US20030096345A1
; GENERAL INFORMATION:
;  APPLICANT: GLUCKSMANN, Maria A
;  TITLE OF INVENTION: 15569, A NOVEL HUMAN G PROTEIN COUPLED RECEPTOR AND USES THEREFOR
;  FILE REFERENCE: 10147-60U1
;  CURRENT APPLICATION NUMBER: US/10/054,044A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/263,253
;  PRIOR FILING DATE: 2001-01-22
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1014
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-054-044A-4

  Query Match            100.0%;  Score 63;  DB 14;  Length 1014;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784
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RESULT 12
US-10-120-604-4
; Sequence 4, Application US/10120604
; Publication No. US20030096347A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPT
; TITLE OF INVENTION: HGPRBMY28 AND HGPRBMY29, AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1014
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-4

Query Match 100.0%; Score 63; DB 14; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 13
US-10-120-604-139
; Sequence 139, Application US/10120604
; Publication No. US20030096347A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPT
; TITLE OF INVENTION: HGPRBMY28 AND HGPRBMY29, AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139
; LENGTH: 1014
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-139

Query Match 100.0%; Score 63; DB 14; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 14
US-10-225-567A-428
; Sequence 428, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 428
; LENGTH: 1014
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-428

Query Match 100.0%; Score 63; DB 14; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 15
US-10-295-027-492
; Sequence 492, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13

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;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 492
;   LENGTH: 1014
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-492

  Query Match           100.0%;  Score 63;  DB 15;  Length 1014;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


RESULT 16
US-10-295-027-810
; Sequence 810, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 810
;   LENGTH: 1014
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-810

  Query Match           100.0%;  Score 63;  DB 15;  Length 1014;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


RESULT 17
US-10-295-027-847
; Sequence 847, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 847
;   LENGTH: 1014
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-847

  Query Match           100.0%;  Score 63;  DB 15;  Length 1014;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


RESULT 18
US-10-173-999-20
; Sequence 20, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
;  APPLICANT: Mack, David H.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
;  TITLE OF INVENTION:  and Methods of Screening for Modulators of Ovarian
;  TITLE OF INVENTION:  Cancer
;  FILE REFERENCE: 018501-002420US
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;  CURRENT APPLICATION NUMBER: US/10/173,999
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: US 60/299,234
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/315,287
;  PRIOR FILING DATE: 2001-08-27
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/372,246
;  PRIOR FILING DATE: 2001-04-12
;  NUMBER OF SEQ ID NOS: 163
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 1014
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-173-999-20

  Query Match           100.0%;  Score 63;  DB 15;  Length 1014;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


RESULT 19
US-10-741-657A-2
; Sequence 2, Application US/10741657A
; Publication No. US20040197325A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
;  FILE REFERENCE: 05882.0177.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/741,657A
;  CURRENT FILING DATE:  2003-12-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 1014
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-741-657A-2

  Query Match           100.0%;  Score 63;  DB 16;  Length 1014;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


RESULT 20
US-10-723-860-2455
; Sequence 2455, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Ginsburg, Wendy M.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;  TITLE OF INVENTION:  Methods for Screening for Soft Tissue Sarcoma Modulators
;  FILE REFERENCE: 05882.0193.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/723,860
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: 60/429,739
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 8393
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2455
;   LENGTH: 1014
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-723-860-2455

  Query Match           100.0%;  Score 63;  DB 16;  Length 1014;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


RESULT 21
US-10-349-528-24
; Sequence 24, Application US/10349528
; Publication No. US20040253668A1
; GENERAL INFORMATION:
;  APPLICANT: RAMANATHAN, Chandra
;  APPLICANT:  GOPAL, Shuba
;  APPLICANT:  MINTIER, Gabe
;  APPLICANT:  FEDER, John
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
;  TITLE OF INVENTION:  USE THEREOF
;  FILE REFERENCE: D0210
;  CURRENT APPLICATION NUMBER: US/10/349,528
;  CURRENT FILING DATE:  2003-01-22
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
;   LENGTH: 1014
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-10-349-528-24

  Query Match           100.0%;  Score 63;  DB 16;  Length 1014;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


RESULT 22
US-11-070-456-4
; Sequence 4, Application US/11070456
; Publication No. US20050148016A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR HGPRBMY29sv1 POLYPEPTIDES
;  FILE REFERENCE: D0143 DIV1
;  CURRENT APPLICATION NUMBER: US/11/070,456
;  CURRENT FILING DATE:  2005-03-02
;  PRIOR APPLICATION NUMBER: US 60/283,145
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: US 10/120,604
;  PRIOR FILING DATE: 2002-04-11
;  PRIOR APPLICATION NUMBER: US 60/283,161
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: US 60/288,468
;  PRIOR FILING DATE: 2001-05-03
;  PRIOR APPLICATION NUMBER: US 60/300,619
;  PRIOR FILING DATE: 2001-06-25
;  NUMBER OF SEQ ID NOS: 226
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 1014
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-070-456-4

  Query Match           100.0%;  Score 63;  DB 20;  Length 1014;
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  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


RESULT 23
US-11-070-456-139
; Sequence 139, Application US/11070456
; Publication No. US20050148016A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR HGPRBMY29sv1 POLYPEPTIDES
;  FILE REFERENCE: D0143 DIV1
;  CURRENT APPLICATION NUMBER: US/11/070,456
;  CURRENT FILING DATE:  2005-03-02
;  PRIOR APPLICATION NUMBER: US 60/283,145
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: US 10/120,604
;  PRIOR FILING DATE: 2002-04-11
;  PRIOR APPLICATION NUMBER: US 60/283,161
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: US 60/288,468
;  PRIOR FILING DATE: 2001-05-03
;  PRIOR APPLICATION NUMBER: US 60/300,619
;  PRIOR FILING DATE: 2001-06-25
;  NUMBER OF SEQ ID NOS: 226
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
;   LENGTH: 1014
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-070-456-139

  Query Match             100.0%;  Score 63;  DB 20;  Length 1014;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


RESULT 24
US-10-668-181-2
; Sequence 2, Application US/10668181
; Publication No. US20050202439A1
;   GENERAL INFORMATION:
;        APPLICANT: OSTERHOFF, CAROLINE
;                   IVELL, RICHARD
;        TITLE OF INVENTION: EPIDIDYMIS-SPECIFIC RECEPTOR PROTEIN
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22201
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/668,181
;             FILING DATE: 24-Sep-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/041,745
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B.J.
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 35-125
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 703-816-4000
;             TELEFAX: 703-816-4100
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1038 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-668-181-2

  Query Match             100.0%;  Score 63;  DB 18;  Length 1038;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        799 CWINNNAVFY 808


RESULT 25
US-10-505-486-38
; Sequence 38, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
;  APPLICANT: Takeda Chemical Industries, Ltd.
;  TITLE OF INVENTION: Determination of a ligand
;  FILE REFERENCE: P03-0006PCT
;  CURRENT APPLICATION NUMBER: US/10/505,486
;  CURRENT FILING DATE:  2004-08-20
;  PRIOR APPLICATION NUMBER: JP 2002-45728
;  PRIOR FILING DATE: 2002-02-22
;  PRIOR APPLICATION NUMBER: JP 2002-213949
;  PRIOR FILING DATE: 2002-07-23
;  PRIOR APPLICATION NUMBER: JP 2002-298237
;  PRIOR FILING DATE: 2002-10-11
;  NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 38
;   LENGTH: 1252
;   TYPE: PRT
;   ORGANISM: Human
US-10-505-486-38

  Query Match             100.0%;  Score 63;  DB 17;  Length 1252;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


Search completed: October 20, 2005, 07:42:32
Job time : 62 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 20, 2005, 05:49:15 ; Search time 21 Seconds
(without alignments)
35.547 Million cell updates/sec

Title: US-10-668-181-6
Perfect score: 63
Sequence: 1 CWINNNAVPY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	65.1	314	4	US-09-107-532A-7216	Sequence 7216, Ap
2	40	63.5	440	4	US-09-054-272-34	Sequence 34, Appl
3	40	63.5	440	4	US-09-919-497-80	Sequence 80, Appl
4	40	63.5	443	4	US-09-949-016-9574	Sequence 9574, Ap
5	39	61.9	541	4	US-09-976-594-931	Sequence 931, App
6	38	60.3	438	2	US-08-846-762-8	Sequence 8, Appli
7	38	60.3	439	4	US-09-252-991A-28726	Sequence 28726, A
8	38	60.3	685	3	US-08-947-965-72	Sequence 72, Appl
9	38	60.3	686	3	US-08-947-965-73	Sequence 73, Appl
10	37	58.7	208	4	US-09-248-796A-17615	Sequence 17615, A
11	37	58.7	222	2	US-08-440-517A-3	Sequence 3, Appli
12	37	58.7	222	3	US-09-092-160-3	Sequence 3, Appli
13	37	58.7	233	4	US-09-112-498A-9	Sequence 9, Appli
14	37	58.7	769	4	US-09-248-796A-16368	Sequence 16368, A
15	37	58.7	1272	4	US-09-543-681A-5732	Sequence 5732, Ap
16	36	57.1	29	2	US-08-637-759B-101	Sequence 101, App
17	36	57.1	29	3	US-08-871-355A-101	Sequence 101, App
18	36	57.1	29	3	US-09-201-945-101	Sequence 101, App
19	36	57.1	118	4	US-09-489-039A-12473	Sequence 12473, A
20	36	57.1	196	3	US-09-134-001C-4649	Sequence 4649, Ap
21	36	57.1	228	2	US-08-440-517A-2	Sequence 2, Appli
22	36	57.1	228	3	US-09-092-160-2	Sequence 2, Appli
23	36	57.1	237	4	US-09-112-498A-7	Sequence 7, Appli
24	36	57.1	238	4	US-09-328-352-5904	Sequence 5904, Ap
25	36	57.1	254	4	US-09-071-252-37	Sequence 37, Appl
26	36	57.1	501	2	US-08-408-095-31	Sequence 31, Appl
27	36	57.1	686	3	US-08-947-965-70	Sequence 70, Appl
28	35	55.6	107	4	US-09-513-999C-6485	Sequence 6485, Ap
29	35	55.6	221	3	US-09-129-030-26	Sequence 26, Appl
30	35	55.6	224	3	US-09-129-030-24	Sequence 24, Appl
31	35	55.6	240	4	US-09-270-767-38489	Sequence 38489, A
32	35	55.6	240	4	US-09-270-767-53706	Sequence 53706, A
33	35	55.6	289	4	US-09-071-035-72	Sequence 72, Appl
34	35	55.6	301	4	US-09-134-000C-6014	Sequence 6014, Ap
35	35	55.6	312	4	US-09-071-035-70	Sequence 70, Appl
36	35	55.6	354	4	US-09-328-352-5540	Sequence 5540, Ap
37	35	55.6	365	4	US-09-801-874-5	Sequence 5, Appli
38	35	55.6	371	4	US-09-902-540-10866	Sequence 10866, A
39	35	55.6	416	4	US-09-949-016-7087	Sequence 7087, Ap
40	35	55.6	511	4	US-09-902-540-15937	Sequence 15937, A
41	35	55.6	590	4	US-09-489-039A-12982	Sequence 12982, A
42	34	54.0	82	4	US-09-248-796A-20781	Sequence 20781, A
43	34	54.0	111	4	US-09-621-976-3934	Sequence 3934, Ap
44	34	54.0	112	4	US-09-621-976-3935	Sequence 3935, Ap
45	34	54.0	131	4	US-09-433-241A-6	Sequence 6, Appli

ALIGNMENTS

```
RESULT 1
US-09-107-532A-7216
; Sequence 7216, Application US/09107532A
; Patent No. 6583275
;  GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;  INFORMATION FOR SEQ ID NO: 7216:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 314 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: YES
;       ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...314
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7216:
US-09-107-532A-7216
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  Query Match            65.1%;  Score 41;  DB 4;  Length 314;
  Best Local Similarity  55.6%;  Pred. No. 49;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              |:||  :||
Db        289 WVNNKRIFY 297


RESULT 2
US-09-054-272-34
; Sequence 34, Application US/09054272
; Patent No. 6692909
;  GENERAL INFORMATION:
;    APPLICANT:  Lander, Eric S.
;    APPLICANT:  Daley, George Q.
;    APPLICANT:  Cargill, Michele
;    APPLICANT:  Ireland, James S.
;    APPLICANT:  Rozen, Steven G.
;    TITLE OF INVENTION:  CODING SEQUENCE POLYMORPHISMS
;    TITLE OF INVENTION:  IN VASCULAR PATHOLOGY GENES
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/054,272
;      FILING DATE:  01-APR-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI98-05
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  781-861-6240
;      TELEFAX:  781-861-9540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  440 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-09-054-272-34

  Query Match            63.5%;  Score 40;  DB 4;  Length 440;
  Best Local Similarity  60.0%;  Pred. No. 1e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         98 CWIDNTRVVY 107


RESULT 3
US-09-919-497-80
; Sequence 80, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
;  APPLICANT: Mutter, George L.
;  TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
;  FILE REFERENCE: B0801/7225
;  CURRENT APPLICATION NUMBER: US/09/919,497
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/221,735
;  PRIOR FILING DATE: 2000-07-31
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
;   LENGTH: 440
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-919-497-80

  Query Match            63.5%;  Score 40;  DB 4;  Length 440;
  Best Local Similarity  60.0%;  Pred. No. 1e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         98 CWIDNTRVVY 107


RESULT 4
US-09-949-016-9574
; Sequence 9574, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9574
;   LENGTH: 443
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9574

  Query Match            63.5%;  Score 40;  DB 4;  Length 443;
  Best Local Similarity  60.0%;  Pred. No. 1e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db        101 CWIDNTRVVY 110


RESULT 5
US-09-976-594-931
; Sequence 931, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
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;  SOFTWARE: PERL Program
; SEQ ID NO 931
;   LENGTH: 541
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 1530186CD1
US-09-976-594-931

  Query Match             61.9%;  Score 39;  DB 4;  Length 541;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||| :  :||
Db        304 CWIQDPVIFY 313


RESULT 6
US-08-846-762-8
; Sequence 8, Application US/08846762A
; Patent No. 5994072
; GENERAL INFORMATION:
;  APPLICANT: Lam, Joseph S.
;  APPLICANT: Burrows, Lori
;  APPLICANT: Charter, Deborah
;  APPLICANT: de Kievit, Teresa
;  TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
;  TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
;  FILE REFERENCE: 6580-089
;  CURRENT APPLICATION NUMBER: US/08/846,762A
;  CURRENT FILING DATE: 1997-04-30
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 438
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-08-846-762-8

  Query Match             60.3%;  Score 38;  DB 2;  Length 438;
  Best Local Similarity   44.4%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              |:||| :::
Db         27 WVNNNYIYH 35


RESULT 7
US-09-252-991A-28726
; Sequence 28726, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 28726
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28726

  Query Match             60.3%;  Score 38;  DB 4;  Length 439;
  Best Local Similarity   44.4%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              |:||| :::
Db         28 WVNNNYIYH 36


RESULT 8
US-08-947-965-72
; Sequence 72, Application US/08947965A
; Patent No. 6004790
; GENERAL INFORMATION:
;  APPLICANT: Dijkhuizen, Lubbert
;  APPLICANT: Dijkstra, Bauke
;  APPLICANT: Andersen, Carsten
;  APPLICANT: Osten, Claus von der
;  TITLE OF INVENTION: Cyclomaltodextrin Glucanotransferase
;  TITLE OF INVENTION: Variants
;  FILE REFERENCE: 4285.204-US
;  CURRENT APPLICATION NUMBER: US/08/947,965A
;  CURRENT FILING DATE: 1997-10-09
;  EARLIER APPLICATION NUMBER: 0477/95
;  EARLIER FILING DATE: 1995-04-21
;  EARLIER APPLICATION NUMBER: 1173/95
;  EARLIER FILING DATE: 1995-10-17
;  EARLIER APPLICATION NUMBER: 1281/95
;  EARLIER FILING DATE: 1995-11-16
;  EARLIER APPLICATION NUMBER: PCT/DK96/00179
;  EARLIER FILING DATE: 1996-04-22
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 72
;   LENGTH: 685
;   TYPE: PRT
;   ORGANISM: Bacillus sp.
US-08-947-965-72

  Query Match             60.3%;  Score 38;  DB 3;  Length 685;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              ||||: : |
Db        413 WINNDVIIY 421


RESULT 9
US-08-947-965-73
; Sequence 73, Application US/08947965A
; Patent No. 6004790
; GENERAL INFORMATION:
;  APPLICANT: Dijkhuizen, Lubbert
;  APPLICANT: Dijkstra, Bauke
;  APPLICANT: Andersen, Carsten
;  APPLICANT: Osten, Claus von der
;  TITLE OF INVENTION: Cyclomaltodextrin Glucanotransferase
;  TITLE OF INVENTION: Variants
;  FILE REFERENCE: 4285.204-US
;  CURRENT APPLICATION NUMBER: US/08/947,965A
;  CURRENT FILING DATE: 1997-10-09
;  EARLIER APPLICATION NUMBER: 0477/95
;  EARLIER FILING DATE: 1995-04-21
;  EARLIER APPLICATION NUMBER: 1173/95
;  EARLIER FILING DATE: 1995-10-17
;  EARLIER APPLICATION NUMBER: 1281/95
;  EARLIER FILING DATE: 1995-11-16
;  EARLIER APPLICATION NUMBER: PCT/DK96/00179
;  EARLIER FILING DATE: 1996-04-22
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
;   LENGTH: 686
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;   TYPE: PRT
;   ORGANISM: Bacillus sp.
US-08-947-965-73

  Query Match            60.3%;  Score 38;  DB 3;  Length 686;
  Best Local Similarity  55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              ||||: : |
Db        413 WINNDVIIY 421


RESULT 10
US-09-248-796A-17615
; Sequence 17615, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17615
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-17615

  Query Match            58.7%;  Score 37;  DB 4;  Length 208;
  Best Local Similarity  40.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||:|:| : :
Db         16 CWVNSNYLVF 25


RESULT 11
US-08-440-517A-3
; Sequence 3, Application US/08440517A
; Patent No. 5959082
;  GENERAL INFORMATION:
;    APPLICANT:  COSGROVE, DANIEL J.;
;    APPLICANT:  GUILTINAN, MARK;
;    APPLICANT:  SHCHERBAN, TATYANA;
;    APPLICANT:  SHI, JUN
;    TITLE OF INVENTION:  PURIFIED EXPANSIN PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INTELLECTUAL PROPERTY OFFICE, THE
;      ADDRESSEE:  PENNSYLVANIA STATE UNIVERSITY
;      STREET:  113 TECHNOLOGY CENTER
;      CITY:  UNIVERSITY PARK
;      STATE:  PENNSYLVANIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  16802-7000
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  NEC 286
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/440,517A
;      FILING DATE:
;      CLASSIFICATION:  530
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  222
;      TYPE:  AMINO ACID
;      TOPOLOGY:  UNKNOWN
US-08-440-517A-3

  Query Match            58.7%;  Score 37;  DB 2;  Length 222;
  Best Local Similarity  66.7%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              ||| :| ||
Db          5 WINAHATFY 13


RESULT 12
US-09-092-160-3
; Sequence 3, Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
;  APPLICANT: Cosgrove, Daniel J
;  APPLICANT: McQueen-Mason, Simon
;  APPLICANT: Guiltinan, Mark J
;  APPLICANT: Shcherban, Tatyana
;  APPLICANT: Shi, Jun
;  TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
;  FILE REFERENCE: 1194/1C114US3
;  CURRENT APPLICATION NUMBER: US/09/092,160C
;  CURRENT FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 08/440,517
;  EARLIER FILING DATE: 1995-05-12
;  EARLIER APPLICATION NUMBER: 08/242,090
;  EARLIER FILING DATE: 1994-05-12
;  EARLIER APPLICATION NUMBER: 08/060,944
;  EARLIER FILING DATE: 1993-05-12
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 222
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: rice expansin
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (14)..(58)
;   OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160-3

  Query Match            58.7%;  Score 37;  DB 3;  Length 222;
  Best Local Similarity  66.7%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              ||| :| ||
Db          5 WINAHATFY 13


RESULT 13
US-09-112-498A-9
; Sequence 9, Application US/09112498A
; Patent No. 6458928
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES
;    TITLE OF INVENTION:  ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH
;    TITLE OF INVENTION:  SWOLLENINS
;    NUMBER OF SEQUENCES:  31
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/112,498A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 98/14226
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/893,766
;      FILING DATE:  11-JUL-1997
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  233 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-09-112-498A-9

  Query Match             58.7%;  Score 37;  DB 4;  Length 233;
  Best Local Similarity   66.7%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              ||| :| ||
Db         16 WINAHATFY 24


RESULT 14
US-09-248-796A-16368
; Sequence 16368, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16368
;   LENGTH: 769
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-16368

  Query Match             58.7%;  Score 37;  DB 4;  Length 769;
  Best Local Similarity   55.6%;  Pred. No. 5.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              ||| | ::|
Db        166 WINKNELYY 174


RESULT 15
US-09-543-681A-5732
; Sequence 5732, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5732
;   LENGTH: 1272
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-5732

  Query Match             58.7%;  Score 37;  DB 4;  Length 1272;
  Best Local Similarity   71.4%;  Pred. No. 9.3e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CWINNNA 7
              ||:| ||
Db        719 CWVNPNA 725


Search completed: October 20, 2005, 05:50:24
Job time : 22 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 20, 2005, 07:25:13 ; Search time 164 Seconds
(without alignments)
23.583 Million cell updates/sec

Title: US-10-668-181-6
Perfect score: 63
Sequence: 1 CWINNNAVFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	63	100.0	328	4	AAM24057	Aam24057 Human EST
2	63	100.0	513	6	ABG73644	Abg73644 Human G-p
3	63	100.0	936	7	ADB80454	Adb80454 Ovarian c
4	63	100.0	936	7	ADN39172	Adn39172 Cancer/an
5	63	100.0	966	8	ADN88596	Adn88596 Human epi
6	63	100.0	967	7	ADB80452	Adb80452 Ovarian c
7	63	100.0	967	7	ADN39170	Adn39170 Cancer/an
8	63	100.0	979	8	ADN88599	Adn88599 Human epi
9	63	100.0	987	8	ADN88607	Adn88607 Human epi
10	63	100.0	993	7	ADB80450	Adb80450 Ovarian c
11	63	100.0	993	8	ADN88601	Adn88601 Human epi
12	63	100.0	995	8	ADN88609	Adn88609 Human epi
13	63	100.0	1000	7	ADB80458	Adb80458 Ovarian c
14	63	100.0	1000	7	ADN39168	Adn39168 Cancer/an
15	63	100.0	1001	8	ADN88605	Adn88605 Human epi
16	63	100.0	1003	8	ADN88603	Adn88603 Human epi
17	63	100.0	1013	3	AAB01247	Aab01247 Human HE6
18	63	100.0	1014	6	ABJ38840	Abj38840 Human G-p
19	63	100.0	1014	6	ABJ38832	Abj38832 Human epi
20	63	100.0	1014	6	ABP81971	Abp81971 Human G p
21	63	100.0	1014	6	ABR61472	Abr61472 Human sec
22	63	100.0	1014	7	ADB80456	Adb80456 Ovarian c
23	63	100.0	1014	7	ADN39174	Adn39174 Cancer/an
24	63	100.0	1014	7	ADN39529	Adn39529 Cancer/an
25	63	100.0	1014	7	ADN39492	Adn39492 Cancer/an
26	63	100.0	1014	7	ADP03579	Adp03579 Human GPC
27	63	100.0	1014	8	ADO29079	Ado29079 Human nov
28	63	100.0	1014	8	ADQ19636	Adq19636 Human sof
29	63	100.0	1014	8	ADQ09616	Adq09616 Human G p
30	63	100.0	1017	8	ADN88592	Adn88592 Human epi
31	63	100.0	1020	8	ADN88597	Adn88597 Human epi
32	63	100.0	1033	8	ADN88598	Adn88598 Human epi
33	63	100.0	1038	2	AAW36903	Aaw36903 Human epi
34	63	100.0	1041	8	ADN88606	Adn88606 Human epi
35	63	100.0	1047	8	ADN88600	Adn88600 Human epi
36	63	100.0	1049	8	ADN88608	Adn88608 Human epi
37	63	100.0	1055	8	ADN88604	Adn88604 Human epi
38	63	100.0	1057	8	ADN88602	Adn88602 Human epi
39	63	100.0	1071	8	ADN88610	Adn88610 Human epi
40	63	100.0	1252	7	ADF70415	Adf70415 Orphan re
41	54	85.7	717	5	AAU99588	Aau99588 Human G p
42	54	85.7	982	8	ADN88617	Adn88617 Mouse epi
43	54	85.7	993	8	ADN88613	Adn88613 Mouse epi
44	54	85.7	1005	8	ADN88616	Adn88616 Mouse epi
45	54	85.7	1006	8	ADN88615	Adn88615 Mouse epi

ALIGNMENTS

RESULT 1
AAM24057
ID AAM24057 standard; protein; 328 AA.
XX
AC AAM24057;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1582.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR N-PSDB; AAH98716.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 20; Page 1081-1082; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention
XX
SQ Sequence 328 AA;

Query Match 100.0%; Score 63; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 89 CWINNNAVFY 98

RESULT 2
ABG73644
ID ABG73644 standard; protein; 513 AA.
XX
AC ABG73644;
XX
DT 11-MAR-2003 (first entry)
XX
DE Human G-protein coupled receptor associated protein SEQ ID 4.
XX
KW G-protein coupled receptor; secretin receptor subfamily; human; GPCR;
KW protease; Parkinson's disease; receptor.
XX
OS Homo sapiens.
XX
PN US2002142951-A1.
XX
PD 03-OCT-2002.
XX
PF 28-MAR-2001; 2001US-00818264.
XX
PR 28-MAR-2001; 2001US-00818264.
XX
PA (WEBS/) WEBSTER M.
PA (BEAS/) BEASLEY E M.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
XX
PI Webster M, Beasley EM, Ketchum KA, Di Francesco V;
XX
DR WPI; 2003-138646/13.
XX
PT New human protease peptides, useful for preparing a composition for
PT treating a disease or condition mediated by human proteases e.g.
PT Parkinson's disease.
XX
PS Disclosure; Fig 2; 84pp; English.
XX
CC This invention describes a novel human G-protein coupled receptor, its
CC allelic variants, orthologs or fragments of the polypeptide. The
CC invention also describes (1) an isolated antibody that selectively binds
CC to the peptide; (2) an isolated nucleic acid comprising a sequence or its
CC complement that hybridizes under stringent conditions to the opposite
CC strand of the sequence encoding the protease or its allelic variant,
CC ortholog or fragment; (3) a gene chip comprising the isolated nucleic
CC acid of (2); (4) a transgenic non-human animal comprising the isolated
CC nucleic acid of (2); (5) a vector comprising the isolated nucleic acid of
CC (2); (6) a host cell containing the vector of (5); (7) a method for
CC producing the novel peptide; (8) detecting the presence of the novel
CC peptide or nucleic acid of (2) in a sample; (9) identifying a modulator
CC of, or an agent that binds to, the novel peptide; (10) a pharmaceutical
CC composition comprising the agent that binds to the novel peptide and a
CC carrier; (11) treating a disease or condition mediated by human proteases
CC ; (12) identifying a modulator of the expression of the novel peptide;
CC and (13) an isolated human protease peptide having a sequence that shares
CC at least 70 % homology with the protease described in the invention. The
CC product of the invention can be used in gene therapy or for preparing a
CC composition for treating a disease or condition mediated by a human
CC protease protein e.g. Parkinson's disease. This sequence represents a
CC protein associated with the human G-protein coupled receptor (GPCR)
CC related to the secretin receptor subfamily, described in the disclosure
CC of the invention
XX
SQ Sequence 513 AA;

Query Match 100.0%; Score 63; DB 6; Length 513;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 379 CWINNNAVFY 388

RESULT 3
ADB80454
ID ADB80454 standard; protein; 936 AA.
XX
AC ADB80454;
XX
DT 04-DEC-2003 (first entry)
XX
DE Ovarian cancer-associated protein #9.
XX
KW cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
KW post-operative chemotherapy; radiation therapy; tumour prognosis;
KW pre-cancerous lesion detection.
XX
OS Homo sapiens.
XX
PN WO2002102235-A2.
XX
PD 27-DEC-2002.
XX
PF 18-JUN-2002; 2002WO-US019297.
XX
PR 18-JUN-2001; 2001US-0299234P.
PR 27-AUG-2001; 2001US-0315287P.
PR 05-SEP-2001; 2001US-0317544P.
PR 13-NOV-2001; 2001US-0350666P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Mack DH, Gish KC;
XX
DR WPI; 2003-167431/16.
DR N-PSDB; ADB80453.
XX
PT Detecting an ovarian cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT polynucleotide that hybridizes to an ovarian cancer gene.
XX
PS Claim 13; Page 280; 332pp; English.
XX
CC The invention relates to a method of detecting an ovarian cancer-
CC associated transcript in a cell from a patient, by contacting a
CC biological sample from the patient with a polynucleotide that selectively
CC hybridizes to a sequence at least 80% identical to any of one of 80
CC nucleic acid sequences given in the specification. The method is useful
CC in diagnosing ovarian cancer and in identifying and using agents and/or
CC targets that inhibit ovarian cancer. The nucleic acid molecule,
CC polypeptide and the antibody may also be used in detecting ovarian
CC cancers, monitoring and early detection of relapse following treatment,
CC monitoring response to therapy, selecting patients for post-operative
CC chemotherapy or radiation therapy, in selecting mode of therapy,
CC determining tumour prognosis, early detection of pre-cancerous lesions,
CC and as vaccines. This sequence corresponds to one of the proteins used
CC for the detection method of the invention.
XX
SQ Sequence 936 AA;

Query Match 100.0%; Score 63; DB 7; Length 936;

```
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        748 CWINNNAVFY 757


RESULT 4
ADN39172
ID   ADN39172 standard; protein; 936 AA.
XX
AC   ADN39172;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:490.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0396839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Ginsburg WM,  Gish KC,  Glynne R,  Hevezi PA;
PI   Mack DH,  Murray R,  Watson SR,  Wilson KE,  Zlotnik A;
XX
DR   WPI; 2003-468649/44.
DR   N-PSDB; ADN39171.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
PT   a nucleic acid in a biological sample.
XX
PS   Claim 12; SEQ ID NO 490; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention or by detecting a polypeptide of the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC   neovascularistaion syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a polypeptide of the invention.
XX
SQ   Sequence 936 AA;

  Query Match             100.0%;  Score 63;  DB 7;  Length 936;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        748 CWINNNAVFY 757


RESULT 5
ADN88596
ID   ADN88596 standard; protein; 966 AA.
XX
AC   ADN88596;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human epididymis-specific receptor protein-6 delta 24 (HE6delta24) #1.
XX
KW   Human epididymis-specific receptor protein-6; HE6;
KW   male reproductive disorder; infertility; antiinfertility; contraceptive;
KW   human epididymis-specific receptor protein-6 delta 24; HE6delta24;
KW   mutant; mutein; receptor.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004037860-A1.
XX
PD   06-MAY-2004.
XX
PF   21-OCT-2003; 2003WO-EP011662.
XX
PR   22-OCT-2002; 2002US-0419979P.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Kirchhoff C,  Obermann-Pless H,  Samalecos A,  Osterhoff C;
PI   Gottwald U,  Nubbemeyer R;
XX
DR   WPI; 2004-357427/33.
DR   N-PSDB; ADN88595.
XX
PT   Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT   polypeptide, useful for isolating agents used for treating male
PT   infertility, or for male contraception.
XX
PS   Claim 55; SEQ ID NO 34; 127pp; English.
XX
CC   The invention relates to the human epididymis-specific receptor protein-6
CC   (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC   polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC   polypeptide. The invention also relates to an antibody or its fragment
CC   specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC   composition comprising an antisense nucleotide which can bind with any of
CC   the nucleotide sequences encoding an epididymis-specific receptor protein
CC   -6 of the invention, a pharmaceutical composition for treating a male
CC   reproductive disorder comprising a polynucleotide of the invention, a
CC   method of diagnosing infertility in a male mammal and a method of
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```
CC   treating infertility in a male mammal. The polynucleotides encoding the
CC   polypeptides are useful for isolating an agent that modulates expression
CC   or activity of the polypeptides. The sequences are useful for diagnosing
CC   a male reproductive disorder. This sequence represents an HE6delta24
CC   mutant polypeptide of the invention.
XX
SQ   Sequence 966 AA;

  Query Match             100.0%;  Score 63;  DB 8;  Length 966;
  Best Local Similarity   100.0%;  Pred. No. 0.18;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        778 CWINNNAVFY 787


RESULT 6
ADB80452
ID   ADB80452 standard; protein; 967 AA.
XX
AC   ADB80452;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Ovarian cancer-associated protein #8.
XX
KW   cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
KW   post-operative chemotherapy; radiation therapy; tumour prognosis;
KW   pre-cancerous lesion detection.
XX
OS   Homo sapiens.
XX
PN   WO2002102235-A2.
XX
PD   27-DEC-2002.
XX
PF   18-JUN-2002; 2002WO-US019297.
XX
PR   18-JUN-2001; 2001US-0299234P.
PR   27-AUG-2001; 2001US-0315287P.
PR   05-SEP-2001; 2001US-0317544P.
PR   13-NOV-2001; 2001US-0350666P.
PR   12-APR-2002; 2002US-0372246P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Mack DH,  Gish KC;
XX
DR   WPI; 2003-167431/16.
DR   N-PSDB; ADB80451.
XX
PT   Detecting an ovarian cancer-associated transcript in a cell from a
PT   patient, comprises contacting a biological sample from the patient with a
PT   polynucleotide that hybridizes to an ovarian cancer gene.
XX
PS   Claim 13; Page 279; 332pp; English.
XX
CC   The invention relates to a method of detecting an ovarian cancer-
CC   associated transcript in a cell from a patient, by contacting a
CC   biological sample from the patient with a polynucleotide that selectively
CC   hybridizes to a sequence at least 80% identical to any of one of 80
CC   nucleic acid sequences given in the specification. The method is useful
CC   in diagnosing ovarian cancer and in identifying and using agents and/or
CC   targets that inhibit ovarian cancer. The nucleic acid molecule,
CC   polypeptide and the antibody may also be used in detecting ovarian
CC   cancers, monitoring and early detection of relapse following treatment,
CC   monitoring response to therapy, selecting patients for post-operative
CC   chemotherapy or radiation therapy, in selecting mode of therapy,
CC   determining tumour prognosis, early detection of pre-cancerous lesions,
CC   and as vaccines. This sequence corresponds to one of the proteins used
CC   for the detection method of the invention.
XX
SQ   Sequence 967 AA;

  Query Match             100.0%;  Score 63;  DB 7;  Length 967;
  Best Local Similarity   100.0%;  Pred. No. 0.18;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        728 CWINNNAVFY 737


RESULT 7
ADN39170
ID   ADN39170 standard; protein; 967 AA.
XX
AC   ADN39170;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:488.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0396839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Ginsburg WM,  Gish KC,  Glynne R,  Hevezi PA;
PI   Mack DH,  Murray R,  Watson SR,  Wilson KE,  Zlotnik A;
XX
DR   WPI; 2003-468649/44.
DR   N-PSDB; ADN39169.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
PT   a nucleic acid in a biological sample.
XX
PS   Claim 12; SEQ ID NO 488; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
```

CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularistaion syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 967 AA;

Query Match 100.0%; Score 63; DB 7; Length 967;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 728 CWINNNAVFY 737

RESULT 8
ADN88599
ID ADN88599 standard; protein; 979 AA.
XX
AC ADN88599;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 (HE6) polypeptide #3.
XX
KW Human epididymis-specific receptor protein-6; HE6;
KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88578.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 58; SEQ ID NO 37; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 979 AA;

Query Match 100.0%; Score 63; DB 8; Length 979;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 740 CWINNNAVFY 749

RESULT 9
ADN88607
ID ADN88607 standard; protein; 987 AA.
XX
AC ADN88607;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 (HE6) polypeptide #11.
XX
KW Human epididymis-specific receptor protein-6; HE6;
KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88582.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 58; SEQ ID NO 45; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 987 AA;

```
  Query Match             100.0%;  Score 63;  DB 8;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0.18;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        748 CWINNNAVFY 757


RESULT 10
ADB80450
ID   ADB80450 standard; protein; 993 AA.
XX
AC   ADB80450;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Ovarian cancer-associated protein #7.
XX
KW   cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
KW   post-operative chemotherapy; radiation therapy; tumour prognosis;
KW   pre-cancerous lesion detection.
XX
OS   Homo sapiens.
XX
PN   WO2002102235-A2.
XX
PD   27-DEC-2002.
XX
PF   18-JUN-2002; 2002WO-US019297.
XX
PR   18-JUN-2001; 2001US-0299234P.
PR   27-AUG-2001; 2001US-0315287P.
PR   05-SEP-2001; 2001US-0317544P.
PR   13-NOV-2001; 2001US-0350666P.
PR   12-APR-2002; 2002US-0372246P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Mack DH,  Gish KC;
XX
DR   WPI; 2003-167431/16.
DR   N-PSDB; ADB80449.
XX
PT   Detecting an ovarian cancer-associated transcript in a cell from a
PT   patient, comprises contacting a biological sample from the patient with a
PT   polynucleotide that hybridizes to an ovarian cancer gene.
XX
PS   Claim 13; Page 278; 332pp; English.
XX
CC   The invention relates to a method of detecting an ovarian cancer-
CC   associated transcript in a cell from a patient, by contacting a
CC   biological sample from the patient with a polynucleotide that selectively
CC   hybridizes to a sequence at least 80% identical to any of one of 80
CC   nucleic acid sequences given in the specification. The method is useful
CC   in diagnosing ovarian cancer and in identifying and using agents and/or
CC   targets that inhibit ovarian cancer. The nucleic acid molecule,
CC   polypeptide and the antibody may also be used in detecting ovarian
CC   cancers, monitoring and early detection of relapse following treatment,
CC   monitoring response to therapy, selecting patients for post-operative
CC   chemotherapy or radiation therapy, in selecting mode of therapy,
CC   determining tumour prognosis, early detection of pre-cancerous lesions,
CC   and as vaccines. This sequence corresponds to one of the proteins used
CC   for the detection method of the invention.
XX
SQ   Sequence 993 AA;

  Query Match             100.0%;  Score 63;  DB 7;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 0.18;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        754 CWINNNAVFY 763


RESULT 11
ADN88601
ID   ADN88601 standard; protein; 993 AA.
XX
AC   ADN88601;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human epididymis-specific receptor protein-6 (HE6) polypeptide #5.
XX
KW   Human epididymis-specific receptor protein-6; HE6;
KW   male reproductive disorder; infertility; antiinfertility; contraceptive;
KW   receptor.
XX
OS   Homo sapiens.
XX
PN   WO2004037860-A1.
XX
PD   06-MAY-2004.
XX
PF   21-OCT-2003; 2003WO-EP011662.
XX
PR   22-OCT-2002; 2002US-0419979P.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Kirchhoff C,  Obermann-Pless H,  Samalecos A,  Osterhoff C;
PI   Gottwald U,  Nubbemeyer R;
XX
DR   WPI; 2004-357427/33.
DR   N-PSDB; ADN88579.
XX
PT   Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT   polypeptide, useful for isolating agents used for treating male
PT   infertility, or for male contraception.
XX
PS   Claim 58; SEQ ID NO 39; 127pp; English.
XX
CC   The invention relates to the human epididymis-specific receptor protein-6
CC   (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC   polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC   polypeptide. The invention also relates to an antibody or its fragment
CC   specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC   composition comprising an antisense nucleotide which can bind with any of
CC   the nucleotide sequences encoding an epididymis-specific receptor protein
CC   -6 of the invention, a pharmaceutical composition for treating a male
CC   reproductive disorder comprising a polynucleotide of the invention, a
CC   method of diagnosing infertility in a male mammal and a method of
CC   treating infertility in a male mammal. The polynucleotides encoding the
CC   polypeptides are useful for isolating an agent that modulates expression
CC   or activity of the polypeptides. The sequences are useful for diagnosing
CC   a male reproductive disorder. This sequence represents an HE6 polypeptide
CC   of the invention.
XX
SQ   Sequence 993 AA;

  Query Match             100.0%;  Score 63;  DB 8;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 0.18;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        754 CWINNNAVFY 763


RESULT 12
ADN88609
ID   ADN88609 standard; protein; 995 AA.
XX
```

AC ADN88609;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 (HE6) polypeptide #13.
XX
KW Human epididymis-specific receptor protein-6; HE6;
KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88583.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 58; SEQ ID NO 47; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 995 AA;

Query Match 100.0%; Score 63; DB 8; Length 995;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 756 CWINNNAVFY 765

RESULT 13
ADB80458
ID ADB80458 standard; protein; 1000 AA.
XX
AC ADB80458;
XX
DT 04-DEC-2003 (first entry)
XX
DE Ovarian cancer-associated protein #11.
XX
KW cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
KW post-operative chemotherapy; radiation therapy; tumour prognosis;
KW pre-cancerous lesion detection.
XX
OS Homo sapiens.
XX
PN WO2002102235-A2.
XX
PD 27-DEC-2002.
XX
PF 18-JUN-2002; 2002WO-US019297.
XX
PR 18-JUN-2001; 2001US-0299234P.
PR 27-AUG-2001; 2001US-0315287P.
PR 05-SEP-2001; 2001US-0317544P.
PR 13-NOV-2001; 2001US-0350666P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Mack DH, Gish KC;
XX
DR WPI; 2003-167431/16.
DR N-PSDB; ADB80457.
XX
PT Detecting an ovarian cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT polynucleotide that hybridizes to an ovarian cancer gene.
XX
PS Claim 13; Page 282; 332pp; English.
XX
CC The invention relates to a method of detecting an ovarian cancer-
CC associated transcript in a cell from a patient, by contacting a
CC biological sample from the patient with a polynucleotide that selectively
CC hybridizes to a sequence at least 80% identical to any of one of 80
CC nucleic acid sequences given in the specification. The method is useful
CC in diagnosing ovarian cancer and in identifying and using agents and/or
CC targets that inhibit ovarian cancer. The nucleic acid molecule,
CC polypeptide and the antibody may also be used in detecting ovarian
CC cancers, monitoring and early detection of relapse following treatment,
CC monitoring response to therapy, selecting patients for post-operative
CC chemotherapy or radiation therapy, in selecting mode of therapy,
CC determining tumour prognosis, early detection of pre-cancerous lesions,
CC and as vaccines. This sequence corresponds to one of the proteins used
CC for the detection method of the invention.
XX
SQ Sequence 1000 AA;

Query Match 100.0%; Score 63; DB 7; Length 1000;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 761 CWINNNAVFY 770

RESULT 14
ADN39168
ID ADN39168 standard; protein; 1000 AA.
XX
AC ADN39168;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:486.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnerary; gene therapy; vaccine.
XX

OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR WPI; 2003-468649/44.
DR N-PSDB; ADN39167.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 12; SEQ ID NO 486; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularistaion syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 1000 AA;

Query Match 100.0%; Score 63; DB 7; Length 1000;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 761 CWINNNAVFY 770

RESULT 15
ADN88605
ID ADN88605 standard; protein; 1001 AA.
XX
AC ADN88605;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 (HE6) polypeptide #9.
XX
KW Human epididymis-specific receptor protein-6; HE6;
KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88581.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 58; SEQ ID NO 43; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 1001 AA;

Query Match 100.0%; Score 63; DB 8; Length 1001;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 762 CWINNNAVFY 771

RESULT 16
ADN88603
ID ADN88603 standard; protein; 1003 AA.
XX
AC ADN88603;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 (HE6) polypeptide #7.
XX
KW Human epididymis-specific receptor protein-6; HE6;

KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88580.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 58; SEQ ID NO 41; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 1003 AA;

Query Match 100.0%; Score 63; DB 8; Length 1003;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 764 CWINNNAVFY 773

RESULT 17
AAB01247
ID AAB01247 standard; protein; 1013 AA.
XX
AC AAB01247;
XX
DT 03-OCT-2000 (first entry)
XX
DE Human HE6 receptor.
XX
KW Human; HE6 receptor; zsig56; seven transmembrane domain receptor;
KW hypotensive; antigout; cytostatic; antiinflammatory; ion homeostasis;
KW cardiant; neurotransmitter; neuroprotective; antiparkinsonian;
KW cerebroprotective; nootropic; neuroleptic; tranquiliser; antiarthritic;
KW reproductive; signal transduction activator; bone disease; hypertension;
KW renal failure; heart failure; hyperthyroidism; hyperparathyroidism;
KW carcinoma; sarcoidosis; pancreatitis; stress; high blood pressure;
KW immune depression; periodontal disease; neurodegenerative disease;
KW multiple sclerosis, Alzheimer's disease; Parkinson's disease;
KW schizophrenia; manic depression; stroke; rheumatoid arthritis;
KW male fertility; spermatogenesis stimulation; pregnancy regulation;
KW prostate cancer.
XX
OS Homo sapiens.
XX
PN WO200034473-A2.
XX
PD 15-JUN-2000.
XX
PF 02-DEC-1999; 99WO-US028492.
XX
PR 10-DEC-1998; 98US-00208691.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Ellsworth JL;
XX
DR WPI; 2000-442164/38.
XX
PT Novel G-protein coupled receptor zsig56 useful for treating hypertension,
PT hyper and hypothyroidism, inflammation, gout, carcinoma, pancreatitis,
PT Alzheimer's disease and Parkinson's disease, renal and heart failure.
XX
PS Disclosure; Fig 1; 121pp; English.
XX
CC The present sequence is the human HE6 receptor, which shows homology to a
CC seven transmembrane domain receptor designated zsig56. The full length
CC nucleotide sequence was obtained from a human retina library. zsig56
CC polypeptides, nucleic acid, agonists and/or antagonists may be used to
CC treat a wide range of disorders including certain bone diseases,
CC hypertension, renal failure, gout, congestive heart failure,
CC hyperthyroidism, hyperparathyroidism, certain carcinomas, sarcoidosis and
CC pancreatitis. They can be used to treat disorders associated with changes
CC in ion or electrolyte homeostasis, and stress induced disorders such as
CC high blood pressure, heart failure, immune depression and periodontal
CC disease. They may be used to treat neurodegenerative diseases, including
CC multiple sclerosis, Alzheimer's disease and Parkinson's disease,
CC schizophrenia and manic depression, and to repair nerve tissue following
CC damage due to strokes and brain and spinal injuries. Inflammatory
CC disorders such as rheumatoid arthritis can also be treated. zsig56 is
CC expressed in tissues associated with reproduction, i.e. the testis,
CC prostate and placenta, and may be used to treat male fertility by
CC stimulating spermatogenesis and to regulate gestation and birth. zsig56
CC may be useful as a marker or therapeutic agent in the treatment of
CC prostate cancer
XX
SQ Sequence 1013 AA;

Query Match 100.0%; Score 63; DB 3; Length 1013;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 774 CWINNNAVFY 783

RESULT 18
ABJ38840
ID ABJ38840 standard; protein; 1014 AA.
XX
AC ABJ38840;
XX
DT 17-SEP-2003 (first entry)
XX
DE Human G-protein coupled receptor HE6 protein SEQ ID 139.
XX
KW Neuroprotective; antiinflammatory; immunosuppressive; cytostatic; neural;
KW nephrotropic; cardiant; human G-protein receptor; HGRBMY28; HGRBMY29;
KW HGPRBMY29v1; HGPRBMY29v2; HGRBMY28; HGRBMY29; immune disorder; pulmonary;
KW inflammatory; haematopoietic; gastrointestinal; small intestine; cancer;
KW proliferative; aberrant p27 regulation; FEN1; cell cycle; DNA repair;

KW apoptosis; spleen; lymph node; reproductive; oesophageal; metabolic;
KW endocrine; colon; cervix; lung; squamous cell; renal; cardiovascular;
KW placental; testis; heart; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200283856-A2.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US011525.
XX
PR 11-APR-2001; 2001US-0283145P.
PR 11-APR-2001; 2001US-0283161P.
PR 03-MAY-2001; 2001US-0288468P.
PR 25-JUN-2001; 2001US-0300619P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Bol D, Feder J, Mintier G, Ramanathan C, Hawken DR;
XX
DR WPI; 2003-075538/07.
XX
PT New G-protein coupled receptors, HGRBMY28 and HGRBMY29, and their
PT variants, useful for treating, preventing or ameliorating e.g.
PT hematopoietic, neural, pulmonary, gastrointestinal, inflammatory or
PT proliferative disorders.
XX
PS Disclosure; Fig 13; 501pp; English.
XX
CC This invention relates to an isolated nucleic acid molecule comprising a
CC polynucleotide encoding a human G-protein receptor, including HGRBMY28,
CC HGRBMY29, HGPRBMY29v1 or HGPRBMY29v2 polypeptides. The HGRBMY28 or
CC HGRBMY29 polypeptides and nucleic acids are useful for treating,
CC preventing or ameliorating a medical condition, e.g. an immune disorder,
CC an inflammatory disorder, an inflammatory disorder in which G-protein
CC coupled receptors are either directly or indirectly associated with the
CC disorder, a haematopoietic disorder, a neural disorder, a pulmonary
CC disorder, a gastrointestinal disorder, a disorder afflicting the small
CC intestine, a proliferative disorder, a cancer, a disorder related to
CC aberrant p27 regulation, a disorder related to aberrant FEN1 regulation,
CC a disorder related to aberrant cell cycle regulation, a disorder related
CC to aberrant DNA repair regulation, a disorder related to aberrant
CC apoptosis regulation, a disorder of the spleen, a disorder of the lymph
CC nodes, a male or female reproductive disorder, an oesophageal disorder, a
CC metabolic disorder, an endocrine disorder, a proliferative disorder
CC afflicting the colon, cervix, lung, squamous cells or tissues, a renal
CC disorder, a cardiovascular disorder, a placental disorder, and a disorder
CC of the testes, heart or lymph nodes. The isolated polynucleotides of the
CC invention may be used to treat disorders by gene therapy. This sequence
CC represents a Human G-protein coupled receptor related protein of the
CC invention
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 6; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 19
ABJ38832
ID ABJ38832 standard; protein; 1014 AA.
XX
AC ABJ38832;
XX
DT 17-SEP-2003 (first entry)
XX
DE Human epididymis-specific G-protein coupled receptor 64 protein SEQ ID 4.
XX
KW Neuroprotective; antiinflammatory; immunosuppressive; cytostatic; neural;
KW nephrotropic; cardiant; human G-protein receptor; HGRBMY28; HGRBMY29;
KW HGPRBMY29v1; HGPRBMY29v2; HGRBMY28; HGRBMY29; immune disorder; pulmonary;
KW inflammatory; haematopoietic; gastrointestinal; small intestine; cancer;
KW proliferative; aberrant p27 regulation; FEN1; cell cycle; DNA repair;
KW apoptosis; spleen; lymph node; reproductive; oesophageal; metabolic;
KW endocrine; colon; cervix; lung; squamous cell; renal; cardiovascular;
KW placental; testis; heart; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200283856-A2.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US011525.
XX
PR 11-APR-2001; 2001US-0283145P.
PR 11-APR-2001; 2001US-0283161P.
PR 03-MAY-2001; 2001US-0288468P.
PR 25-JUN-2001; 2001US-0300619P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Bol D, Feder J, Mintier G, Ramanathan C, Hawken DR;
XX
DR WPI; 2003-075538/07.
XX
PT New G-protein coupled receptors, HGRBMY28 and HGRBMY29, and their
PT variants, useful for treating, preventing or ameliorating e.g.
PT hematopoietic, neural, pulmonary, gastrointestinal, inflammatory or
PT proliferative disorders.
XX
PS Disclosure; Fig 2; 501pp; English.
XX
CC This invention relates to an isolated nucleic acid molecule comprising a
CC polynucleotide encoding a human G-protein receptor, including HGRBMY28,
CC HGRBMY29, HGPRBMY29v1 or HGPRBMY29v2 polypeptides. The HGRBMY28 or
CC HGRBMY29 polypeptides and nucleic acids are useful for treating,
CC preventing or ameliorating a medical condition, e.g. an immune disorder,
CC an inflammatory disorder, an inflammatory disorder in which G-protein
CC coupled receptors are either directly or indirectly associated with the
CC disorder, a haematopoietic disorder, a neural disorder, a pulmonary
CC disorder, a gastrointestinal disorder, a disorder afflicting the small
CC intestine, a proliferative disorder, a cancer, a disorder related to
CC aberrant p27 regulation, a disorder related to aberrant FEN1 regulation,
CC a disorder related to aberrant cell cycle regulation, a disorder related
CC to aberrant DNA repair regulation, a disorder related to aberrant
CC apoptosis regulation, a disorder of the spleen, a disorder of the lymph
CC nodes, a male or female reproductive disorder, an oesophageal disorder, a
CC metabolic disorder, an endocrine disorder, a proliferative disorder
CC afflicting the colon, cervix, lung, squamous cells or tissues, a renal
CC disorder, a cardiovascular disorder, a placental disorder, and a disorder
CC of the testes, heart or lymph nodes. The isolated polynucleotides of the
CC invention may be used to treat disorders by gene therapy. This sequence
CC represents a Human G-protein coupled receptor related protein of the
CC invention
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 6; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 20
ABP81971
ID ABP81971 standard; protein; 1014 AA.

XX
AC ABP81971;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human G protein-coupled receptor GPR64 protein SEQ ID NO:428.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR N-PSDB; ABZ42819.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 6; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 21
ABR61472
ID ABR61472 standard; protein; 1014 AA.
XX
AC ABR61472;
XX
DT 17-SEP-2003 (first entry)
XX
DE Human secretin-like G-protein coupled receptor (latrophilin #3.
XX
KW GPCR; secretin-type G-protein coupled receptor; latrophilin; cardiant;
KW G-protein coupled receptor; cytostatic; anorectic; antidiabetic;
KW neuroprotective; gene therapy; central nervous system; haematological;
KW genitourological; cardiovascular; obesity; diabetes; cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003051925-A1.
XX
PD 26-JUN-2003.
XX
PF 19-DEC-2002; 2002WO-EP014572.
XX
PR 19-DEC-2001; 2001US-0340825P.
PR 30-AUG-2002; 2002US-0406984P.
XX
PA (FARB) BAYER AG.
XX
PI Koehler RH;
XX
DR WPI; 2003-514042/48.
XX
PT New isolated polynucleotide, useful for preparing a medicament for
PT modulating the activity of secretin-type GPCR (latrophilin) polypeptide
PT in a disease, e.g., cardiovascular disease, obesity, diabetes or cancer.
XX
PS Disclosure; Page 155-158; 161pp; English.
XX
CC The invention relates to a novel isolated polynucleotide comprising e.g.
CC a sequence encoding a secretin-type G-protein coupled receptor (GPCR)
CC (latrophilin) polypeptide. A protein of the invention has cytostatic,
CC cardiant, anorectic, antidiabetic, and neuroprotective activity. The
CC polynucleotide may have a use in gene therapy. The expression vector is
CC useful for preparing a medicament for modulating the activity of secretin
CC -type GPCR (latrophilin) polypeptide in a disease, e.g., central nervous
CC system, haematological, genitourological or cardiovascular disease,
CC obesity, diabetes or cancer. The present sequence represents a secretin-
CC type GPCR (latrophilin) polypeptide of the invention
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 6; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 22
ADB80456
ID ADB80456 standard; protein; 1014 AA.
XX
AC ADB80456;
XX

DT 04-DEC-2003 (first entry)
XX
DE Ovarian cancer-associated protein #10.
XX
KW cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
KW post-operative chemotherapy; radiation therapy; tumour prognosis;
KW pre-cancerous lesion detection.
XX
OS Homo sapiens.
XX
PN WO2002102235-A2.
XX
PD 27-DEC-2002.
XX
PF 18-JUN-2002; 2002WO-US019297.
XX
PR 18-JUN-2001; 2001US-0299234P.
PR 27-AUG-2001; 2001US-0315287P.
PR 05-SEP-2001; 2001US-0317544P.
PR 13-NOV-2001; 2001US-0350666P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Mack DH, Gish KC;
XX
DR WPI; 2003-167431/16.
DR N-PSDB; ADB80455.
XX
PT Detecting an ovarian cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT polynucleotide that hybridizes to an ovarian cancer gene.
XX
PS Claim 13; Page 281; 332pp; English.
XX
CC The invention relates to a method of detecting an ovarian cancer-
CC associated transcript in a cell from a patient, by contacting a
CC biological sample from the patient with a polynucleotide that selectively
CC hybridizes to a sequence at least 80% identical to any of one of 80
CC nucleic acid sequences given in the specification. The method is useful
CC in diagnosing ovarian cancer and in identifying and using agents and/or
CC targets that inhibit ovarian cancer. The nucleic acid molecule,
CC polypeptide and the antibody may also be used in detecting ovarian
CC cancers, monitoring and early detection of relapse following treatment,
CC monitoring response to therapy, selecting patients for post-operative
CC chemotherapy or radiation therapy, in selecting mode of therapy,
CC determining tumour prognosis, early detection of pre-cancerous lesions,
CC and as vaccines. This sequence corresponds to one of the proteins used
CC for the detection method of the invention.
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 7; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 23
ADN39174
ID ADN39174 standard; protein; 1014 AA.
XX
AC ADN39174;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:492.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnerary; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR WPI; 2003-468649/44.
DR N-PSDB; ADN39173.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 12; SEQ ID NO 492; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularistaion syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 7; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||

```
Db        775 CWINNNAVFY 784

RESULT 24
ADN39529
ID   ADN39529 standard; protein; 1014 AA.
XX
AC   ADN39529;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A129.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0396839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Ginsburg WM,  Gish KC,  Glynne R,  Hevezi PA;
PI   Mack DH,  Murray R,  Watson SR,  Wilson KE,  Zlotnik A;
XX
DR   WPI; 2003-468649/44.
DR   N-PSDB; ADN39528.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
PT   a nucleic acid in a biological sample.
XX
PS   Claim 12; SEQ ID NO A129; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention or by detecting a polypeptide of the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC   neovascularistaion syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a polypeptide of the invention.
XX
SQ   Sequence 1014 AA;

  Query Match            100.0%;  Score 63;  DB 7;  Length 1014;
  Best Local Similarity  100.0%;  Pred. No. 0.19;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784


RESULT 25
ADN39492
ID   ADN39492 standard; protein; 1014 AA.
XX
AC   ADN39492;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A92.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0396839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Ginsburg WM,  Gish KC,  Glynne R,  Hevezi PA;
PI   Mack DH,  Murray R,  Watson SR,  Wilson KE,  Zlotnik A;
XX
DR   WPI; 2003-468649/44.
DR   N-PSDB; ADN39491.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
```

PT a nucleic acid in a biological sample.
XX
PS Claim 12; SEQ ID NO A92; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularistaion syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 7; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 26
ADP03579
ID ADP03579 standard; protein; 1014 AA.
XX
AC ADP03579;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human GPCR HE6 (GPCR 64, epididymis-specific) protein.
XX
KW GPCR; G-protein coupled receptor; neuroprotective; nootropic;
KW tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant;
KW anticonvulsant; antiparkinsonian; cytostatic; cardiant; hypotensive;
KW antianginal; analgesic; anorectic; anti-HIV; antiasthmatic; osteopathic;
KW uropathic; antiulcer; antiallergic; cell cycle regulation; neurological;
KW severe mental retardation; dyskinesia; brain; spinal cord; affective;
KW neoplastic; cardiovascular; immunological; immune; endocrinal; growth;
KW eating; HIV infection; cancer; metabolic; pituitary;
KW chromosome identification; gene therapy; human; receptor; HE6;
KW GPCR 64 epididymis-specific.
XX
OS Homo sapiens.
XX
PN WO2003062393-A2.
XX
PD 31-JUL-2003.
XX
PF 22-JAN-2003; 2003WO-US001911.
XX
PR 22-JAN-2002; 2002US-0350724P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Ramanathan CS, Gopal S, Mintier G, Feder JN;
XX
DR WPI; 2003-618283/58.
XX
PT New nucleic acid molecule encoding a human G-protein coupled receptor,
PT useful for diagnosing, preventing or treating diseases involving the
PT receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
PT cancer.
XX
PS Example 1; SEQ ID NO 24; 224pp; English.
XX
CC The invention relates to a novel isolated GPCR (G-protein coupled
CC receptor) nucleic acid molecule. The polynucleotide and polypeptide of
CC the invention demonstrate neuroprotective, nootropic, tranquiliser,
CC antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,
CC antiparkinsonian, cytostatic, cardiant, hypotensive, antianginal,
CC analgesic, anorectic, anti-HIV, antiasthmatic, osteopathic, uropathic,
CC antiulcer and antiallergic properties. The nucleic acid molecule and
CC polypeptide of the invention may be useful in diagnosing, preventing,
CC treating or ameliorating a medical condition, such as a disorder related
CC to aberrant G-protein coupled signalling, a disorder related to aberrant
CC cell cycle regulation, neurological disorders, severe mental retardation
CC and dyskinesias, brain disorders, spinal cord disorders, affective
CC disorders, neoplastic disorders, cardiovascular disorders, immunological
CC disorders, immune-related disorders, endocrinal diseases, growth
CC disorders, eating disorders, HIV infection, cancers, metabolic disorders
CC and pituitary disorders. Furthermore, the polynucleotide may be used in
CC chromosome identification, in identifying organisms from minute
CC biological samples, in gene therapy or as a molecular weight marker. The
CC current sequence is that of a human GPCR (G-protein coupled receptor)
CC protein of the invention which was used for homology purposes.
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 7; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 27
ADO29079
ID ADO29079 standard; protein; 1014 AA.
XX
AC ADO29079;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human novel GPCR GPR64, SEQ ID NO:178.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX

PA (PRIM-) PRIMAL INC.
XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
DR WPI; 2004-390329/36.
DR N-PSDB; ADO29771.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 1; SEQ ID NO 178; 542pp; English.
XX
CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the trasngenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 8; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 28
ADQ19636
ID ADQ19636 standard; protein; 1014 AA.
XX
AC ADQ19636;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2455.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 2455; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 8; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 29
ADQ09616
ID ADQ09616 standard; protein; 1014 AA.
XX
AC ADQ09616;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human G protein coupled receptor GPR64 DNA SeqID 2.
XX
KW human; G protein coupled receptor; GPR64; cytotoxic; ovarian cancer;
KW uterine cancer; Ewing's sarcoma; cell death; cytostatic; gene therapy;
KW immunotherapy; cellular proliferation.
XX
OS Homo sapiens.
XX
PN WO2004058171-A2.
XX
PD 15-JUL-2004.
XX
PF 19-DEC-2003; 2003WO-US040820.
XX
PR 20-DEC-2002; 2002US-0435618P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Law D, Wang Q, Dubridge R, Bhaskar V;
XX

DR WPI; 2004-525780/50.
DR N-PSDB; ADQ09615.
XX
PT New antibody that inhibits binding of a GPR64 polypeptide to an antibody
PT comprising GPR64-18, GPR64-81, GPR64-93 or GPR64-101, useful in preparing
PT a composition for diagnosing or treating ovarian cancer.
XX
PS Claim 31; SEQ ID NO 2; 75pp; English.
XX
CC This invention relates to novel antibodies that bind to the G protein
CC coupled receptor protein identified as GPR64, namely GPR64-1, GPR64-16,
CC GPR64-18, GPR64-20 and GPR64-48. Specifically, it refers to the use of
CC these anti-GPR64 antibodies as selective cytotoxic agents against GPR64
CC expressing tumour cells such as those associated with ovarian cancer,
CC uterine cancer and Ewing's sarcoma. The present invention describes
CC epitope mapping of those antibodies that show high affinity binding to
CC GPR64 through competitive binding analyses, such that the antibodies can
CC be assessed for GPR64 dependent cell death in vitro. Accordingly, they
CC can be used to develop cytostatic compositions for gene therapy or
CC immunotherapy that inhibit cellular proliferation of an ovarian cancerous
CC cell and furthermore can diagnose and inhibit growth of tumour cells.
CC This polypeptide sequence is the target human GPR64 protein of the
CC invention.
XX
SQ Sequence 1014 AA;

Query Match 100.0%; Score 63; DB 8; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 775 CWINNNAVFY 784

RESULT 30
ADN88592
ID ADN88592 standard; protein; 1017 AA.
XX
AC ADN88592;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 (HE6) polypeptide #1.
XX
KW Human epididymis-specific receptor protein-6; HE6;
KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88584.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 4; SEQ ID NO 30; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 1017 AA;

Query Match 100.0%; Score 63; DB 8; Length 1017;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 778 CWINNNAVFY 787

RESULT 31
ADN88597
ID ADN88597 standard; protein; 1020 AA.
XX
AC ADN88597;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 delta 24 (HE6delta24) #2.
XX
KW Human epididymis-specific receptor protein-6; HE6;
KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW human epididymis-specific receptor protein-6 delta 24; HE6delta24;
KW mutant; mutein; receptor.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88595.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 55; SEQ ID NO 35; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of

CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6delta24
CC mutant polypeptide of the invention.
XX
SQ Sequence 1020 AA;

Query Match 100.0%; Score 63; DB 8; Length 1020;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 832 CWINNNAVFY 841

RESULT 32
ADN88598
ID ADN88598 standard; protein; 1033 AA.
XX
AC ADN88598;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 (HE6) polypeptide #2.
XX
KW Human epididymis-specific receptor protein-6; HE6;
KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88578.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 58; SEQ ID NO 36; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 1033 AA;

Query Match 100.0%; Score 63; DB 8; Length 1033;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 794 CWINNNAVFY 803

RESULT 33
AAW36903
ID AAW36903 standard; protein; 1038 AA.
XX
AC AAW36903;
XX
DT 11-MAY-1998 (first entry)
XX
DE Human epididymis-specific receptor protein.
XX
KW Epididymis-specific receptor protein; transmembrane protein;
KW sperm maturation; male infertility; agonist; antagonist; contraception;
KW autoantibody; diagnostic; detection; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1. .1038
FT /note= "partial protein sequence"
XX
PN DE19617940-A1.
XX
PD 30-OCT-1997.
XX
PF 29-APR-1996; 96DE-01017940.
XX
PR 29-APR-1996; 96DE-01017940.
XX
PA (IHFH-) IHF INST HORMON & FORTPFLANZUNGS.
XX
PI Osterhoff C, Ivell R;
XX
DR WPI; 1997-527841/49.
DR N-PSDB; AAT97955.
XX
PT DNA encoding epididymis-specific receptor protein - useful for developing
PT male infertility or contraceptive treatments.
XX
PS Claim 1; Page 19-22; 33pp; German.
XX
CC This sequence represents a novel epididymis-specific receptor protein
CC which is a transmembrane protein associated with the epididymis
CC epithelium and is closely connected with sperm maturation. The protein or
CC its derivative or fragments may be useful for detecting autoantibodies in
CC the serum of infertile men and for developing ligands specific for the
CC receptor, e.g. agonists that may stimulate sperm maturation and thus be
CC useful for treating male infertility or antagonists that may be useful
CC for contraception. The antibodies can be used to detect the receptor in
CC vitro or in vivo. Oligonucleotides derived from the DNA sequences can be
CC used as diagnostic probes
XX
SQ Sequence 1038 AA;

Query Match 100.0%; Score 63; DB 2; Length 1038;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 799 CWINNNAVFY 808

```
RESULT 34
ADN88606
ID   ADN88606 standard; protein; 1041 AA.
XX
AC   ADN88606;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human epididymis-specific receptor protein-6 (HE6) polypeptide #10.
XX
KW   Human epididymis-specific receptor protein-6; HE6;
KW   male reproductive disorder; infertility; antiinfertility; contraceptive;
KW   receptor.
XX
OS   Homo sapiens.
XX
PN   WO2004037860-A1.
XX
PD   06-MAY-2004.
XX
PF   21-OCT-2003; 2003WO-EP011662.
XX
PR   22-OCT-2002; 2002US-0419979P.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Kirchhoff C,  Obermann-Pless H,  Samalecos A,  Osterhoff C;
PI   Gottwald U,  Nubbemeyer R;
XX
DR   WPI; 2004-357427/33.
DR   N-PSDB; ADN88582.
XX
PT   Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT   polypeptide, useful for isolating agents used for treating male
PT   infertility, or for male contraception.
XX
PS   Claim 58; SEQ ID NO 44; 127pp; English.
XX
CC   The invention relates to the human epididymis-specific receptor protein-6
CC   (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC   polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC   polypeptide. The invention also relates to an antibody or its fragment
CC   specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC   composition comprising an antisense nucleotide which can bind with any of
CC   the nucleotide sequences encoding an epididymis-specific receptor protein
CC   -6 of the invention, a pharmaceutical composition for treating a male
CC   reproductive disorder comprising a polynucleotide of the invention, a
CC   method of diagnosing infertility in a male mammal and a method of
CC   treating infertility in a male mammal. The polynucleotides encoding the
CC   polypeptides are useful for isolating an agent that modulates expression
CC   or activity of the polypeptides. The sequences are useful for diagnosing
CC   a male reproductive disorder. This sequence represents an HE6 polypeptide
CC   of the invention.
XX
SQ   Sequence 1041 AA;

  Query Match             100.0%;  Score 63;  DB 8;  Length 1041;
  Best Local Similarity   100.0%;  Pred. No. 0.19;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        802 CWINNNAVFY 811


RESULT 35
ADN88600
ID   ADN88600 standard; protein; 1047 AA.
XX
AC   ADN88600;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human epididymis-specific receptor protein-6 (HE6) polypeptide #4.
XX
KW   Human epididymis-specific receptor protein-6; HE6;
KW   male reproductive disorder; infertility; antiinfertility; contraceptive;
KW   receptor.
XX
OS   Homo sapiens.
XX
PN   WO2004037860-A1.
XX
PD   06-MAY-2004.
XX
PF   21-OCT-2003; 2003WO-EP011662.
XX
PR   22-OCT-2002; 2002US-0419979P.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Kirchhoff C,  Obermann-Pless H,  Samalecos A,  Osterhoff C;
PI   Gottwald U,  Nubbemeyer R;
XX
DR   WPI; 2004-357427/33.
DR   N-PSDB; ADN88579.
XX
PT   Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT   polypeptide, useful for isolating agents used for treating male
PT   infertility, or for male contraception.
XX
PS   Claim 58; SEQ ID NO 38; 127pp; English.
XX
CC   The invention relates to the human epididymis-specific receptor protein-6
CC   (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC   polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC   polypeptide. The invention also relates to an antibody or its fragment
CC   specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC   composition comprising an antisense nucleotide which can bind with any of
CC   the nucleotide sequences encoding an epididymis-specific receptor protein
CC   -6 of the invention, a pharmaceutical composition for treating a male
CC   reproductive disorder comprising a polynucleotide of the invention, a
CC   method of diagnosing infertility in a male mammal and a method of
CC   treating infertility in a male mammal. The polynucleotides encoding the
CC   polypeptides are useful for isolating an agent that modulates expression
CC   or activity of the polypeptides. The sequences are useful for diagnosing
CC   a male reproductive disorder. This sequence represents an HE6 polypeptide
CC   of the invention.
XX
SQ   Sequence 1047 AA;

  Query Match             100.0%;  Score 63;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 0.19;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        808 CWINNNAVFY 817


RESULT 36
ADN88608
ID   ADN88608 standard; protein; 1049 AA.
XX
AC   ADN88608;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human epididymis-specific receptor protein-6 (HE6) polypeptide #12.
XX
KW   Human epididymis-specific receptor protein-6; HE6;
KW   male reproductive disorder; infertility; antiinfertility; contraceptive;
KW   receptor.
XX
```

OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88583.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 58; SEQ ID NO 46; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 1049 AA;

Query Match 100.0%; Score 63; DB 8; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 810 CWINNNAVFY 819

RESULT 37
ADN88604
ID ADN88604 standard; protein; 1055 AA.
XX
AC ADN88604;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 (HE6) polypeptide #8.
XX
KW Human epididymis-specific receptor protein-6; HE6;
KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88581.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 58; SEQ ID NO 42; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 1055 AA;

Query Match 100.0%; Score 63; DB 8; Length 1055;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 816 CWINNNAVFY 825

RESULT 38
ADN88602
ID ADN88602 standard; protein; 1057 AA.
XX
AC ADN88602;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 (HE6) polypeptide #6.
XX
KW Human epididymis-specific receptor protein-6; HE6;
KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.

DR N-PSDB; ADN88580.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 58; SEQ ID NO 40; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 1057 AA;

Query Match 100.0%; Score 63; DB 8; Length 1057;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 818 CWINNNAVFY 827

RESULT 39
ADN88610
ID ADN88610 standard; protein; 1071 AA.
XX
AC ADN88610;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human epididymis-specific receptor protein-6 (HE6) polypeptide #14.
XX
KW Human epididymis-specific receptor protein-6; HE6;
KW male reproductive disorder; infertility; antiinfertility; contraceptive;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004037860-A1.
XX
PD 06-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-EP011662.
XX
PR 22-OCT-2002; 2002US-0419979P.
XX
PA (SCHD) SCHERING AG.
XX
PI Kirchhoff C, Obermann-Pless H, Samalecos A, Osterhoff C;
PI Gottwald U, Nubbemeyer R;
XX
DR WPI; 2004-357427/33.
DR N-PSDB; ADN88584.
XX
PT Novel isolated human, mouse or rat epididymis-specific receptor protein-6
PT polypeptide, useful for isolating agents used for treating male
PT infertility, or for male contraception.
XX
PS Claim 58; SEQ ID NO 48; 127pp; English.
XX
CC The invention relates to the human epididymis-specific receptor protein-6
CC (HE6) polypeptide, the mouse epididymis-specific receptor protein-6 (ME6)
CC polypeptide and the rat epididymis-specific receptor protein-6 (RE6)
CC polypeptide. The invention also relates to an antibody or its fragment
CC specific for the HE6, ME6 or RE6 polypeptide, a pharmaceutical
CC composition comprising an antisense nucleotide which can bind with any of
CC the nucleotide sequences encoding an epididymis-specific receptor protein
CC -6 of the invention, a pharmaceutical composition for treating a male
CC reproductive disorder comprising a polynucleotide of the invention, a
CC method of diagnosing infertility in a male mammal and a method of
CC treating infertility in a male mammal. The polynucleotides encoding the
CC polypeptides are useful for isolating an agent that modulates expression
CC or activity of the polypeptides. The sequences are useful for diagnosing
CC a male reproductive disorder. This sequence represents an HE6 polypeptide
CC of the invention.
XX
SQ Sequence 1071 AA;

Query Match 100.0%; Score 63; DB 8; Length 1071;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CWINNNAVFY 10
||||||||||
Db 832 CWINNNAVFY 841

RESULT 40
ADF70415
ID ADF70415 standard; protein; 1252 AA.
XX
AC ADF70415;
XX
DT 12-FEB-2004 (first entry)
XX
DE Orphan receptor ligand-related human protein SeqID38.
XX
KW ligand; orphan receptor protein; fusion protein; fluorescent protein;
KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
KW GFPuv; Enhanced GFP; EGFP; human.
XX
OS Homo sapiens.
XX
PN WO2003071272-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003WO-JP001901.
XX
PR 22-FEB-2002; 2002JP-00045728.
PR 23-JUL-2002; 2002JP-00213949.
PR 11-OCT-2002; 2002JP-00298237.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
XX
DR WPI; 2003-697654/66.
DR N-PSDB; ADF70517.
XX
PT Transformation of cells with a fusion protein of an orphan receptor
PT protein with a fluorescent protein useful for identification of ligands
PT to the orphan receptor.
XX
PS Disclosure; SEQ ID NO 38; 594pp; Japanese.
XX
CC This invention relates to a novel method of identifying ligands to an
CC orphan receptor protein which comprises transforming cells with DNA
CC encoding a fusion protein of the orphan receptor with a fluorescent
CC protein, so that the fusion protein is expressed in the cells (or cell
CC membranes isolated from them) and contacting the cells with the potential
CC ligand to be tested. A suitable fluorescent protein for incorporation in
CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,

CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
CC identification of ligands binding to an orphan receptor protein.
XX
SQ Sequence 1252 AA;

Query Match 100.0%; Score 63; DB 7; Length 1252;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CWINNNAVFY 10
              ||||||||||
Db        775 CWINNNAVFY 784
```

Search completed: October 20, 2005, 07:41:25
Job time : 166 secs

OM protein - protein search, using sw model

Run on: October 20, 2005, 05:49:15 ; Search time 22 Seconds
(without alignments)
43.735 Million cell updates/sec

Title: US-10-668-181-6
Perfect score: 63
Sequence: 1 CWINNNAVFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	74.6	621	2	T22904	hypothetical prote
2	41	65.1	534	2	S44886	ZK112.1 protein -
3	40	63.5	413	2	I50662	lecithin-cholester
4	40	63.5	440	1	XXHUN	phosphatidylcholin
5	40	63.5	440	1	XXRTN	phosphatidylcholin
6	40	63.5	440	2	JC1502	phosphatidylcholin
7	39	61.9	204	2	S22616	hypothetical prote
8	39	61.9	438	1	XXMSN	phosphatidylcholin
9	39	61.9	564	2	A96999	pectate lyase rela
10	39	61.9	590	2	I40608	cspA protein - Clo
11	39	61.9	635	2	S57714	cspB protein - Clo
12	38.5	61.1	559	1	JQ2010	transcription fact
13	38	60.3	162	2	G95998	probable acetyltra
14	38	60.3	355	2	T12032	NADH2 dehydrogenas
15	38	60.3	355	2	T12031	NADH2 dehydrogenas
16	38	60.3	355	2	T12033	NADH2 dehydrogenas
17	38	60.3	438	2	S77588	O-antigen polymera
18	38	60.3	438	2	D83251	B-band O-antigen p
19	38	60.3	575	2	S72283	DNA-directed RNA p
20	38	60.3	712	1	ALBSG3	cyclomaltodextrin
21	38	60.3	713	1	ALBSG1	cyclomaltodextrin
22	38	60.3	2817	2	B97033	uncharacterized pr
23	37	58.7	255	2	T50655	expansin EXP5 [imp
24	37	58.7	258	2	T48247	expansin-like prot
25	37	58.7	375	2	AC1350	N-acetylmuramoyl-L
26	37	58.7	395	2	S28606	St11p protein - fi
27	37	58.7	490	2	D84998	low-affinity inorg
28	37	58.7	677	2	T11231	NADH2 dehydrogenas
29	37	58.7	778	2	T31037	hypothetical prote
30	37	58.7	867	2	D82940	conserved hypothet
31	37	58.7	1032	1	G7BPT4	baseplate protein
32	37	58.7	1104	1	A36866	microbial collagen
33	36.5	57.9	114	2	B81005	hypothetical prote
34	36.5	57.9	1672	2	T46237	hypothetical prote
35	36	57.1	156	2	A70922	hypothetical prote
36	36	57.1	169	2	F84716	hypothetical prote
37	36	57.1	237	2	T50654	expansin EXP1 [imp
38	36	57.1	248	2	C84444	probable expansin
39	36	57.1	336	2	T22285	hypothetical prote
40	36	57.1	353	2	F69957	hypothetical prote
41	36	57.1	430	2	I48755	mSAP1a - mouse
42	36	57.1	435	2	A64376	amino acid transpo
43	36	57.1	437	2	E84619	probable serine ca
44	36	57.1	483	2	A97295	fusion of Uroporph
45	36	57.1	490	2	A46391	cAMP receptor subt

ALIGNMENTS

RESULT 1
T22904
hypothetical protein F58B4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22904
R;Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19634
A;Accession: T22904
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-621 <WIL>
A;Cross-references: UNIPROT:Q20975; EMBL:Z74038; PIDN:CAA98497.1; GSPDB:GN00023; CESP:F5
A;Experimental source: clone F58B4
C;Genetics:
A;Gene: CESP:F58B4.1
A;Map position: 5
A;Introns: 47/3; 94/3; 135/2; 157/1; 185/1; 218/3; 253/3; 328/1; 366/3; 447/2; 511/2; 58

Query Match 74.6%; Score 47; DB 2; Length 621;
Best Local Similarity 70.0%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CWINNNAVFY 10
              ||:|||  ||
Db        612 CWMNNNNNFY 621
```

RESULT 2
S44886
ZK112.1 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S44886
R;Du, Z.
submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid ZK112.
A;Reference number: S44616
A;Accession: S44886
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-534 <DUZ>
A;Cross-references: UNIPROT:P34610; EMBL:L14324; NID:g289740; PID:g289741
C;Genetics:
A;Introns: 25/3; 65/2; 196/2; 249/1; 275/1; 385/2; 415/2
C;Superfamily: Caenorhabditis elegans ZK688.6 protein

Query Match 65.1%; Score 41; DB 2; Length 534;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 WINNNAVF 9
              |:||| ||
Db        254 WLNNNTVF 261
```

RESULT 3
I50662
lecithin-cholesterol acyltransferase - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50662
R;Hengstschlager-Ottnad, E.; Kuchler, K.; Schneider, W.J.
J. Biol. Chem. 270, 26139-26145, 1995
A;Title: Chicken Lecithin-Cholesterol Acyltransferase. Molecular Characterization reveal
A;Reference number: I50662; MUID:96064680; PMID:7592817
A;Accession: I50662
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-413 <HEN>
A;Cross-references: UNIPROT:P53760; EMBL:X91011; NID:g1050479; PIDN:CAA62493.1; PID:g105
C;Superfamily: phosphatidylcholine-sterol acyltransferase

```
  Query Match             63.5%;  Score 40;  DB 2;  Length 413;
  Best Local Similarity   60.0%;  Pred. No. 32;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         96 CWIDNTRVVY 105
```

RESULT 4
XXHUN
phosphatidylcholine-sterol O-acyltransferase (EC 2.3.1.43) precursor [validated] - human
N;Alternate names: lecithin-cholesterol acyltransferase precursor; phospholipid-choleste
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A00571; A25575; A29661; JQ0036; A29133; I52260; A28511
R;McLean, J.; Fielding, C.; Drayna, D.; Dieplinger, H.; Baer, B.; Kohr, W.; Henzel, W.;
Proc. Natl. Acad. Sci. U.S.A. 83, 2335-2339, 1986
A;Title: Cloning and expression of human lecithin-cholesterol acyltransferase cDNA.
A;Reference number: A00571; MUID:86205950; PMID:3458198
A;Accession: A00571
A;Molecule type: mRNA
A;Residues: 1-440 <MCL1>
A;Cross-references: UNIPROT:P04180; GB:M12625; NID:g187022; PIDN:AAA59498.1; PID:g307117
R;McLean, J.; Wion, K.; Drayna, D.; Fielding, C.; Lawn, R.
Nucleic Acids Res. 14, 9397-9406, 1986
A;Title: Human lecithin-cholesterol acyltransferase gene: complete gene sequence and sit
A;Reference number: A25575; MUID:87091568; PMID:3797244
A;Accession: A25575
A;Molecule type: DNA
A;Residues: 1-440 <MCL2>
A;Cross-references: GB:X04981; NID:g34286; PIDN:CAA28651.1; PID:g34287
R;Rogne, S.; Skretting, G.; Larsen, F.; Myklebost, O.; Mevag, B.; Carlson, L.A.; Holmqui
Biochem. Biophys. Res. Commun. 148, 161-169, 1987
A;Title: The isolation and characterisation of a cDNA clone for human lecithin:cholester
A;Reference number: A29661; MUID:88049652; PMID:2823801
A;Accession: A29661
A;Molecule type: mRNA
A;Residues: 13-440 <ROG>
A;Cross-references: GB:M17959; NID:g187026; PIDN:AAA59500.1; PID:g386858
R;Tata, F.; Chaves, M.E.; Markham, A.F.; Scrace, G.D.; Waterfield, M.D.; McIntyre, N.; W
Biochim. Biophys. Acta 910, 142-148, 1987
A;Title: The isolation and characterisation of cDNA and genomic clones for human lecithi
A;Reference number: A90666; MUID:88050946; PMID:2823898
A;Accession: JQ0036
A;Molecule type: mRNA
A;Residues: 17-256,'H',258-440 <TAT>
A;Cross-references: GB:X06537; NID:g34284; GB:M26268; NID:g187024; PIDN:AAA59499.1; PID:
A;Note: the authors translated the codon CAT for residue 241 as Ile and CAG for residues
R;Yang, C.; Manoogian, D.; Pao, Q.; Lee, F.; Knapp, R.D.; Gotto Jr., A.M.; Pownall, H.J.
J. Biol. Chem. 262, 3086-3091, 1987
A;Title: Lecithin: cholesterol acyltransferase. Functional regions and a structural mode
A;Reference number: A29133; MUID:87137578; PMID:2880847
A;Accession: A29133
A;Molecule type: protein
A;Residues: 25-284,'Q',286-333,'Q',335-440 <YAN>
R;Bujo, H.; Kusunoki, J.; Ogasawara, M.; Yamamoto, T.; Ohta, Y.; Shimada, T.; Saito, Y.;
Biochem. Biophys. Res. Commun. 181, 933-940, 1991
A;Title: Molecular defect in familial lecithin:cholesterol acyltransferase (LCAT) defici
A;Reference number: I52260; MUID:92109783; PMID:1662503
A;Accession: I52260
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 25-34,'AHHAQG' <BUJ>
A;Cross-references: GB:S74079; NID:g241428; PIDN:AAB20750.1; PID:g241429
A;Note: defective frame shift mutant sequence
R;Schindler, P.A.; Settineri, C.A.; Collet, X.; Fielding, C.J.; Burlingame, A.L.
Protein Sci. 4, 791-803, 1995
A;Title: Site-specific detection and structural characterization of the glycosylation of
pectrometry and sequential glycosidase digestion.
A;Reference number: A57914; MUID:95338133; PMID:7613477
A;Contents: annotation; peptide sequences; N- and O-glycosylation
C;Comment: Apolipoprotein A-I (see PIR:LPHUA1) is a potent activator of this enzyme.
C;Genetics:
A;Gene: GDB:LCAT
A;Cross-references: GDB:119359; OMIM:245900
A;Map position: 16q22.1-16q22.1
C;Function:
A;Description: catalyzes the transfer of sn-2 fatty acyl groups from phosphatidylcholine
A;Note: palmitoyl, oleoyl, and linoleoyl residues can be transferred; a number of sterol
C;Superfamily: phosphatidylcholine-sterol acyltransferase
C;Keywords: acyltransferase; cholesterol; glycoprotein; lipid metabolism; lipoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-440/Product: phosphatidylcholine-sterol acyltransferase #status experimental <MAT>
F;202-207/Region: interfacial lipid recognition (GXSXG) motif
F;44,108,296,408/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;431/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;433/Binding site: carbohydrate (Ser) (covalent) #status experimental

```
  Query Match             63.5%;  Score 40;  DB 1;  Length 440;
  Best Local Similarity   60.0%;  Pred. No. 34;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         98 CWIDNTRVVY 107
```

RESULT 5
XXRTN
phosphatidylcholine-sterol O-acyltransferase (EC 2.3.1.43) precursor - rat
N;Alternate names: lecithin-cholesterol acyltransferase precursor; phospholipid-cholester
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S11214; S11302
R;Meroni, G.; Malgaretti, N.; Magnaghi, P.; Taramelli, R.
Nucleic Acids Res. 18, 5308, 1990
A;Title: Nucleotide sequence of the cDNA for lecithin-cholesterol acyl transferase (LCAT)
A;Reference number: S11214; MUID:90384859; PMID:2402469
A;Accession: S11214
A;Molecule type: mRNA
A;Residues: 1-440 <MER>
A;Cross-references: UNIPROT:P18424; EMBL:X54096
R;Taramelli, R.
submitted to the EMBL Data Library, July 1990
A;Reference number: S11302
A;Accession: S11302
A;Molecule type: mRNA
A;Residues: 1-389,'G',391-440 <TAR>
A;Cross-references: EMBL:X54096; NID:g56563; PIDN:CAA38030.1; PID:g56564
C;Comment: The active enzyme catalyzes the transfer of acyl groups from lecithin to sterc
cluding cholesterol, can act as acceptor. Apolipoprotein A-I is a potent activator for th
C;Genetics:
A;Gene: LCAT

```
C;Superfamily: phosphatidylcholine-sterol acyltransferase
C;Keywords: acyltransferase; glycoprotein; lipid metabolism; lipoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-438/Product: phosphatidylcholine-sterol acyltransferase #status predicted <MAT>
F;44,108,296,408/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             63.5%;  Score 40;  DB 1;  Length 440;
  Best Local Similarity   60.0%;  Pred. No. 34;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         98 CWIDNTRVVY 107


RESULT 6
JC1502
phosphatidylcholine-sterol O-acyltransferase (EC 2.3.1.43) precursor - baboon
N;Alternate names: lecithin-cholesterol acyltransferase
C;Species: Papio sp. (baboon)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 03-Jun-2002
C;Accession: JC1502
R;Hixson, J.E.; Driscoll, D.M.; Birnbaum, S.; Britten, M.L.
Gene 128, 295-299, 1993
A;Title: Baboon lecithin cholesterol acyltransferase (LCAT): cDNA sequences of two allel
A;Reference number: JC1502; MUID:93293002; PMID:8514197
A;Accession: JC1502
A;Molecule type: mRNA
A;Residues: 1-440 <HIX>
A;Cross-references: GB:L08633; NID:g176591; PIDN:AAA35388.1; PID:g176592
C;Comment: This enzyme is a key enzyme of cholesterol metabolism that catalyzes esterifi
C;Genetics:
A;Gene: LCAT
C;Superfamily: phosphatidylcholine-sterol acyltransferase
C;Keywords: acyltransferase
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-440/Product: phosphatidylcholine-sterol O-acyltransferase #status predicted <PPC>

  Query Match             63.5%;  Score 40;  DB 2;  Length 440;
  Best Local Similarity   60.0%;  Pred. No. 34;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         98 CWIDNTRVVY 107


RESULT 7
S22616
hypothetical protein 14.9 - Salmonella choleraesuis
C;Species: Salmonella choleraesuis
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 22-Oct-1999
C;Accession: S22616
R;Brown, P.K.; Romana, L.K.; Reeves, P.R.
Mol. Microbiol. 6, 1385-1394, 1992
A;Title: Molecular analysis of the rfb gene cluster of Salmonella serovar muenchen (stra
A;Reference number: S22613; MUID:92349966; PMID:1379320
A;Accession: S22616
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-204 <BRO>
A;Cross-references: EMBL:X61917; NID:g47004; PIDN:CAA43910.1; PID:g47008
C;Superfamily: galactoside acetyltransferase

  Query Match             61.9%;  Score 39;  DB 2;  Length 204;
  Best Local Similarity   75.0%;  Pred. No. 23;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CWINNNAV 8
              ||| :|||
Db        156 CWIGDNAV 163


RESULT 8
XXMSN
phosphatidylcholine-sterol O-acyltransferase (EC 2.3.1.43) precursor - mouse
N;Alternate names: lecithin-cholesterol acyltransferase precursor; phospholipid-choleste
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A34158; S21370
R;Warden, C.H.; Langner, C.A.; Gordon, J.I.; Taylor, B.A.; McLean, J.W.; Lusis, A.J.
J. Biol. Chem. 264, 21573-21581, 1989
A;Title: Tissue-specific expression, developmental regulation, and chromosomal mapping o
A;Reference number: A34158; MUID:90094326; PMID:2600083
A;Accession: A34158
A;Molecule type: mRNA
A;Residues: 1-438 <WAR>
A;Cross-references: UNIPROT:P16301; GB:J05154; NID:g198759; PIDN:AAA39419.1; PID:g293697
A;Note: the authors translated the codon ATG for residue 411 as Leu
R;Meroni, G.; Malgaretti, N.; Magnaghi, P.; Taramelli, R.
submitted to the EMBL Data Library, July 1990
A;Description: Promoter and 5' flanking sequences of the mouse LCAT gene.
A;Reference number: S21370
A;Accession: S21370
A;Molecule type: DNA
A;Residues: 1-14 <MER>
A;Cross-references: EMBL:X54095; NID:g52873; PIDN:CAA38029.1; PID:g52874
C;Comment: The active enzyme catalyzes the transfer of acyl groups from lecithin to ster
cluding cholesterol, can act as acceptor. Apolipoprotein A-I is a potent activator for t
C;Superfamily: phosphatidylcholine-sterol acyltransferase
C;Keywords: acyltransferase; glycoprotein; lipid metabolism; lipoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-438/Product: phosphatidylcholine-sterol acyltransferase #status predicted <MAT>
F;44,108,296,408/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             61.9%;  Score 39;  DB 1;  Length 438;
  Best Local Similarity   50.0%;  Pred. No. 50;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  : |
Db         98 CWIDNTRIVY 107


RESULT 9
A96999
pectate lyase related protein, secreted [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: A96999
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A96999
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-564 <KUR>
A;Cross-references: UNIPROT:Q97KW2; GB:AE001437; PIDN:AAK78780.1; PID:g15023693; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0804

  Query Match             61.9%;  Score 39;  DB 2;  Length 564;
  Best Local Similarity   55.6%;  Pred. No. 64;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              |::|| :||
Db        299 WVHNNDLFY 307


RESULT 10
I40608
cspA protein - Clostridium acetobutylicum
```

```
C;Species: Clostridium acetobutylicum
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40608; S49255
R;Sanchez-Beato, A.R.; Ronda, C.; Garcia, J.L.
J. Bacteriol. 177, 1098-1103, 1995
A;Title: Tracking the evolution of the bacterial choline-binding domain: molecular chara
A;Reference number: I40607; MUID:95164512; PMID:7860591
A;Accession: I40608
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-590 <RES>
A;Cross-references: UNIPROT:Q45819; EMBL:Z37723; NID:g550295; PIDN:CAA85778.1; PID:g5502
C;Genetics:
A;Gene: cspA
F;501-520/Domain: cpl repeat homology <CP1>
F;521-540/Domain: cpl repeat homology <CP2>
F;541-560/Domain: cpl repeat homology <CP3>

  Query Match             61.9%;  Score 39;  DB 2;  Length 590;
  Best Local Similarity   55.6%;  Pred. No. 67;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              |:|:|  ||
Db        554 WLNDNGTFY 562


RESULT 11
S57714
cspB protein - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57714
R;Sanchez-Beato, A.; Garcia, J.
submitted to the EMBL Data Library, July 1995
A;Description: Molecular characterization of a family of choline-binding proteins of Clo
A;Reference number: S57714
A;Accession: S57714
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-635 <SAN>
A;Cross-references: UNIPROT:Q45820; EMBL:Z50008; NID:g895756; PIDN:CAA90303.1; PID:g8957
F;522-541/Domain: cpl repeat homology <CP1>
F;542-561/Domain: cpl repeat homology <CP2>
F;602-621/Domain: cpl repeat homology <CP3>

  Query Match             61.9%;  Score 39;  DB 2;  Length 635;
  Best Local Similarity   55.6%;  Pred. No. 72;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              |:|||  :|
Db        575 WLNNNGTWY 583


RESULT 12
JQ2010
transcription factor POU-1 - planarian (Dugesia japonica)
C;Species: Dugesia japonica
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JQ2010
R;Orii, H.; Agata, K.; Watanabe, K.
Biochem. Biophys. Res. Commun. 192, 1395-1402, 1993
A;Title: POU-domain genes in planarian Dugesia japonica: the structure and expression.
A;Reference number: JQ2010; MUID:93282851; PMID:8099480
A;Accession: JQ2010
A;Molecule type: mRNA
A;Residues: 1-559 <ORI>
A;Cross-references: UNIPROT:P31370; DDBJ:D12924; NID:g217311; PIDN:BAA02308.1; PID:g2173
A;Experimental source: strain GI
C;Genetics:
A;Gene: DjPOU1
C;Superfamily: planarian transcription factor POU-1; homeobox homology; POU domain homol
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;266-333/Domain: POU domain homology <POU>
F;352-408/Domain: homeobox homology <HOX>

  Query Match             61.1%;  Score 38.5;  DB 1;  Length 559;
  Best Local Similarity   53.8%;  Pred. No. 77;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          1 CWINNNAV---FY 10
              || |||  :   ||
Db        148 CWSNNNYIRDDFY 160


RESULT 13
G95998
probable acetyltransferase protein [imported] - Sinorhizobium meliloti (strain 1021) mag
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95998
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G95998
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-162 <KUR>
A;Cross-references: UNIPROT:Q92U82; GB:AL591985; PIDN:CAC49655.1; PID:g15141142; GSPDB:GN
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.(
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb21427
A;Genome: plasmid

  Query Match             60.3%;  Score 38;  DB 2;  Length 162;
  Best Local Similarity   50.0%;  Pred. No. 26;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |::|:  |||
Db         54 CYVNSGCVFY 63


RESULT 14
T12032
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 (isolate Mt. Khumaratkhok Russia) -
C;Species: mitochondrion Carabus cribratus
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T12032
R;Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.
Elytra 26, 223-248, 1998
A;Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on endop
A;Reference number: Z17381
A;Accession: T12032
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <IMU>
A;Cross-references: UNIPROT:O79580; EMBL:AB017461; PIDN:BAA33177.1
A;Experimental source: isolate Mt. Khumaratkhok Russia; adult; thorax muscle
C;Genetics:
A;Genome: mitochondrion
A;Note: ND5
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
```

```
  Query Match             60.3%;  Score 38;  DB 2;  Length 355;
  Best Local Similarity   55.6%;  Pred. No. 59;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              |::|: |||
Db        260 WVSNSLVFY 268


RESULT 15
T12031
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus cribratus mitochondrion
C;Species: mitochondrion Carabus cribratus
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T12031
R;Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.
Elytra 26, 223-248, 1998
A;Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on endo
A;Reference number: Z17381
A;Accession: T12031
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <IMU>
A;Cross-references: UNIPROT:O79579; EMBL:AB017460; PIDN:BAA33176.1
A;Experimental source: isolate Artvin Turkey; adult; thorax muscle
C;Genetics:
A;Genome: mitochondrion
A;Note: ND5
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

  Query Match             60.3%;  Score 38;  DB 2;  Length 355;
  Best Local Similarity   55.6%;  Pred. No. 59;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              |::|: |||
Db        260 WVSNSLVFY 268


Search completed: October 20, 2005, 05:49:54
Job time : 26 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 20, 2005, 05:49:15 ; Search time 55 Seconds
(without alignments)
93.105 Million cell updates/sec

Title: US-10-668-181-6
Perfect score: 63
Sequence: 1 CWINNNAVFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	63	100.0	1017	1	GP64_HUMAN	Q8izp9 homo sapien
2	54	85.7	1009	1	GP64_MOUSE	Q8cj12 mus musculu
3	49	77.8	1013	1	GP64_RAT	Q8cj11 rattus norv
4	47	74.6	578	2	Q20975	Q20975 caenorhabdi
5	44	69.8	566	2	Q6CSG6	Q6csg6 kluyveromyc
6	43	68.3	2799	1	G112_HUMAN	Q8izf6 homo sapien
7	42	66.7	128	2	Q8IFE2	Q8ife2 trypanosoma
8	42	66.7	168	2	Q9LQW3	Q9lqw3 arabidopsis
9	42	66.7	268	2	Q9EPE5	Q9epe5 calomyscus
10	42	66.7	779	2	Q7RLD7	Q7rld7 plasmodium
11	41	65.1	105	2	Q70UX2	Q70ux2 graphiurus
12	41	65.1	125	2	Q70UX6	Q70ux6 dryomys lan
13	41	65.1	126	2	Q70UX1	Q70ux1 graphiurus
14	41	65.1	136	2	Q70UW9	Q70uw9 graphiurus
15	41	65.1	136	2	Q70UX0	Q70ux0 graphiurus
16	41	65.1	136	2	Q70UX3	Q70ux3 graphiurus
17	41	65.1	136	2	Q70UX4	Q70ux4 graphiurus
18	41	65.1	136	2	Q70UX7	Q70ux7 eliomys mel
19	41	65.1	141	2	Q9GLR5	Q9glr5 erinaceus e
20	41	65.1	191	2	Q64SF1	Q64sf1 bacteroides
21	41	65.1	282	2	Q832C2	Q832c2 enterococcu
22	41	65.1	297	2	O35591	O35591 myoxus glis
23	41	65.1	299	1	LCAT_ELIQU	O35573 eliomys que
24	41	65.1	565	1	PCP1_CAEEL	P34610 caenorhabdi
25	41	65.1	572	2	Q7RFI0	Q7rfi0 plasmodium
26	40	63.5	124	2	Q70UX5	Q70ux5 myomimus ro
27	40	63.5	134	2	O08942	O08942 octodon lun
28	40	63.5	134	2	Q70UW8	Q70uw8 aplodontia
29	40	63.5	135	2	Q9ESE7	Q9ese7 cavia porce
30	40	63.5	138	2	O08935	O08935 microtus ni
31	40	63.5	140	2	O08944	O08944 peromyscus
32	40	63.5	148	2	Q9GLR6	Q9glr6 didelphis m
33	40	63.5	201	2	Q811E4	Q811e4 mus musculu
34	40	63.5	209	2	Q8HZA0	Q8hza0 macaca sp.
35	40	63.5	209	2	Q8HZA1	Q8hza1 pongo pygma
36	40	63.5	256	2	Q9EPC9	Q9epc9 sicista kaz
37	40	63.5	258	2	Q9EPE4	Q9epe4 deomys ferr
38	40	63.5	264	2	Q9EPD6	Q9epd6 macrotarsom
39	40	63.5	264	2	Q9EPE7	Q9epe7 acomys cahi
40	40	63.5	265	2	Q91YB3	Q91yb3 saccostomus
41	40	63.5	265	2	Q9EPD7	Q9epd7 mesocricetu
42	40	63.5	266	2	Q9EPC8	Q9epc8 steatomys s
43	40	63.5	267	2	Q9EPC7	Q9epc7 uranomys ru
44	40	63.5	267	2	Q9EPE0	Q9epe0 jaculus jac
45	40	63.5	268	2	Q91YH4	Q91yh4 cricetomys

ALIGNMENTS

```
RESULT 1
GP64_HUMAN
ID   GP64_HUMAN     STANDARD;      PRT;  1017 AA.
AC   Q8IZP9; O00406; Q8IWT2; Q8IZE4; Q8IZE5; Q8IZE6; Q8IZE7; Q8IZP3;
AC   Q8IZP4;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   G protein-coupled receptor 64 precursor (Epididymis-specific protein
DE   6) (He6 receptor).
GN   Name=GPR64; Synonyms=HE6, TM7LN2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Epididymis;
RX   MEDLINE=97294669; PubMed=9150425;
RA   Osterhoff C., Ivell R., Kirchhoff C.;
RT   "Cloning of a human epididymis-specific mRNA, HE6, encoding a novel
RT   member of the seven transmembrane-domain receptor superfamily.";
RL   DNA Cell Biol. 16:379-389(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6; 7; 8 AND 9).
RC   TISSUE=Epididymis;
RX   MEDLINE=22307585; PubMed=12420295; DOI=10.1002/mrd.10220;
RA   Obermann H., Samalecos A., Osterhoff C., Schroeder B., Heller R.,
RA   Kirchhoff C.;
RT   "HE6, a two-subunit heptahelical receptor associated with apical
RT   membranes of efferent and epididymal duct epithelia.";
RL   Mol. Reprod. Dev. 64:13-26(2003).
CC   -!- FUNCTION: Could be involved in a signal transduction pathway
CC       controlling epidymal function and male fertility.
CC   -!- SUBUNIT: Forms a heterodimer, consisting of a large extracellular
CC       region linked to a seven-transmembrane moiety (Probable).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=9;
CC       Name=1; Synonyms=Long splice variant;
CC         IsoId=Q8IZP9-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q8IZP9-2; Sequence=VSP_009791;
CC       Name=3; Synonyms=d1;
CC         IsoId=Q8IZP9-3; Sequence=VSP_009792;
CC       Name=4; Synonyms=24;
CC         IsoId=Q8IZP9-4; Sequence=VSP_009793;
CC       Name=5; Synonyms=23;
CC         IsoId=Q8IZP9-5; Sequence=VSP_009794;
CC       Name=6; Synonyms=d3;
CC         IsoId=Q8IZP9-6; Sequence=VSP_009795;
CC       Name=7; Synonyms=d2;
CC         IsoId=Q8IZP9-7; Sequence=VSP_009796;
CC       Name=8; Synonyms=21;
```

```
CC         IsoId=Q8IZP9-8; Sequence=VSP_009797;
CC       Name=9; Synonyms=Delta exon 28;
CC         IsoId=Q8IZP9-9; Sequence=VSP_009798;
CC   -!- TISSUE SPECIFICITY: Epididymys specific. Both subunits were
CC       associated with apical membranes of efferent ductule and proximal
CC       epididymal duct epithelia.
CC   -!- PTM: Proteolytically cleaved into 2 subunits, an extracellular
CC       subunit and a seven-transmembrane subunit (Potential).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
CC       LN-TM7 subfamily.
CC   -!- SIMILARITY: Contains 1 GPS domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X81892; CAA57479.1; -.
DR   EMBL; AF538954; AAN33056.1; -.
DR   EMBL; AF539455; AAN33064.1; -.
DR   EMBL; AF539456; AAN33065.1; -.
DR   EMBL; AY143364; AAN38971.1; -.
DR   EMBL; AY143365; AAN38972.1; -.
DR   EMBL; AY143366; AAN38973.1; -.
DR   EMBL; AY143367; AAN38974.1; -.
DR   EMBL; AY148343; AAN75702.1; -.
DR   Genew; HGNC:4516; GPR64.
DR   MIM; 602657; -.
DR   InterPro; IPR000832; GPCR_secretin.
DR   InterPro; IPR000203; PKD_cys_rich.
DR   Pfam; PF00002; 7tm_2; 1.
DR   Pfam; PF01825; GPS; 1.
DR   PRINTS; PR00249; GPCRSECRETIN.
DR   SMART; SM00303; GPS; 1.
DR   PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
DR   PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
DR   PROSITE; PS50221; GPS; 1.
KW   Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW   Signal; Transmembrane.
FT   SIGNAL        1     37       Potential.
FT   CHAIN        38   1017       G protein-coupled receptor 64.
FT   DOMAIN       38    627       Extracellular (Potential).
FT   TRANSMEM    628    648       1 (Potential).
FT   DOMAIN      649    667       Cytoplasmic (Potential).
FT   TRANSMEM    668    688       2 (Potential).
FT   DOMAIN      689    693       Extracellular (Potential).
FT   TRANSMEM    694    714       3 (Potential).
FT   DOMAIN      715    737       Cytoplasmic (Potential).
FT   TRANSMEM    738    758       4 (Potential).
FT   DOMAIN      759    789       Extracellular (Potential).
FT   TRANSMEM    790    810       5 (Potential).
FT   DOMAIN      811    834       Cytoplasmic (Potential).
FT   TRANSMEM    835    855       6 (Potential).
FT   DOMAIN      856    857       Extracellular (Potential).
FT   TRANSMEM    858    878       7 (Potential).
FT   DOMAIN      879   1017       Cytoplasmic (Potential).
FT   DOMAIN      672    677       Poly-Leu.
FT   DOMAIN      816    819       Poly-Lys.
FT   DOMAIN      925    930       Poly-Ser.
FT   DOMAIN      567    618       GPS.
FT   CARBOHYD     44     44       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     85     85       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     99     99       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    111    111       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    117    117       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    144    144       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    162    162       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    186    186       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    194    194       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    357    357       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    370    370       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    435    435       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    438    438       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    456    456       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    461    461       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    528    528       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    542    542       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    547    547       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    551    551       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    597    597       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    857    857       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC     65     67       Missing (in isoform 2).
FT                                 /FTId=VSP_009791.
FT   VARSPLIC     51     66       Missing (in isoform 3).
FT                                 /FTId=VSP_009792.
FT   VARSPLIC     88    101       Missing (in isoform 4).
FT                                 /FTId=VSP_009793.
FT   VARSPLIC     52     75       Missing (in isoform 5).
FT                                 /FTId=VSP_009794.
FT   VARSPLIC     68    101       EVETTSLNDVTLSLLPSNETEKTKITIVKTFNAS -> DVT
FT                                 LSLLPSNET (in isoform 6).
FT                                 /FTId=VSP_009795.
FT   VARSPLIC     52    101       AKLSVVSFAPSSNGTPEVETTSLNDVTLSLLPSNETEKTKI
FT                                 TIVKTFNAS -> EVETTSLNDVTLSLLPSNET (in
FT                                 isoform 7).
FT                                 /FTId=VSP_009796.
FT   VARSPLIC     52    101       AKLSVVSFAPSSNGTPEVETTSLNDVTLSLLPSNETEKTKI
FT                                 TIVKTFNAS -> DVTLSLLPSNET (in isoform 8).
FT                                 /FTId=VSP_009797.
FT   VARSPLIC    906    956       Missing (in isoform 9).
FT                                 /FTId=VSP_009798.
SQ   SEQUENCE   1017 AA;  111491 MW;  5CB31B0EE76434BB CRC64;

  Query Match             100.0%;  Score 63;  DB 1;  Length 1017;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||||||||
Db        778 CWINNNAVFY 787


RESULT 2
GP64_MOUSE
ID   GP64_MOUSE     STANDARD;      PRT;  1009 AA.
AC   Q8CJI2; Q8BL10; Q8CJ08; Q8CJ09; Q8CJ10;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   G protein-coupled receptor 64 precursor (Epididymis-specific protein
DE   6) (Me6 receptor).
GN   Name=Gpr64; Synonyms=Me6;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 4 AND 5).
RC   STRAIN=NMRI; TISSUE=Epididymis;
RX   MEDLINE=22307585; PubMed=12420295; DOI=10.1002/mrd.10220;
RA   Obermann H., Samalecos A., Osterhoff C., Schroeder B., Heller R.,
RA   Kirchhoff C.;
RT   "HE6, a two-subunit heptahelical receptor associated with apical
RT   membranes of efferent and epididymal duct epithelia.";
RL   Mol. Reprod. Dev. 64:13-26(2003).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
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RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
CC   -!- FUNCTION: Could be involved in a signal transduction pathway
CC       controlling epidymal function and male fertility.
CC   -!- SUBUNIT: Forms a heterodimer, consisting of a large extracellular
CC       region linked to a seven-transmembrane moiety (Probable).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=5;
CC       Name=1; Synonyms=Long;
CC         IsoId=Q8CJ12-1; Sequence=Displayed;
CC       Name=2; Synonyms=d2;
CC         IsoId=Q8CJ12-2; Sequence=VSP_009808;
CC       Name=3; Synonyms=d1;
CC         IsoId=Q8CJ12-3; Sequence=VSP_009809;
CC       Name=4; Synonyms=d3;
CC         IsoId=Q8CJ12-4; Sequence=VSP_009807;
CC       Name=5;
CC         IsoId=Q8CJ12-5; Sequence=VSP_009806;
CC   -!- TISSUE SPECIFICITY: Epididymys-specific expression. Both subunits
CC       were associated with apical membranes of efferent ductule and
CC       proximal epididymal duct epithelia.
CC   -!- PTM: Proteolytically cleaved into 2 subunits, an extracellular
CC       subunit and a seven-transmembrane subunit (Potential).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
CC       LN-TM7 subfamily.
CC   -!- SIMILARITY: Contains 1 GPS domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF538952; AAN33054.1; -.
DR   EMBL; AF538955; AAN33057.1; -.
DR   EMBL; AF538956; AAN33058.1; -.
DR   EMBL; AF538957; AAN33059.1; -.
DR   EMBL; AK046871; BAC32902.1; -.
DR   MGD; MGI:2446854; Gpr64.
DR   InterPro; IPR000832; GPCR_secretin.
DR   InterPro; IPR000203; PKD_cys_rich.
DR   Pfam; PF00002; 7tm_2; 1.
DR   Pfam; PF01825; GPS; 1.
DR   PRINTS; PR00249; GPCRSECRETIN.
DR   SMART; SM00303; GPS; 1.
DR   PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
DR   PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
DR   PROSITE; PS50221; GPS; 1.
KW   Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW   Signal; Transmembrane.
FT   SIGNAL        1     37       Potential.
FT   CHAIN        38   1009       G protein-coupled receptor 64.
FT   DOMAIN       38    619       Extracellular (Potential).
FT   TRANSMEM    620    640       1 (Potential).
FT   DOMAIN      641    659       Cytoplasmic (Potential).
FT   TRANSMEM    660    680       2 (Potential).
FT   DOMAIN      681    683       Extracellular (Potential).
FT   TRANSMEM    684    704       3 (Potential).
FT   DOMAIN      705    729       Cytoplasmic (Potential).
FT   TRANSMEM    730    750       4 (Potential).
FT   DOMAIN      751    781       Extracellular (Potential).
FT   TRANSMEM    782    802       5 (Potential).
FT   DOMAIN      803    826       Cytoplasmic (Potential).
FT   TRANSMEM    827    847       6 (Potential).
FT   DOMAIN      848    849       Extracellular (Potential).
FT   TRANSMEM    850    870       7 (Potential).
FT   DOMAIN      871   1009       Cytoplasmic (Potential).
FT   DOMAIN      559    610       GPS.
FT   DOMAIN      248    251       Poly-Ser.
FT   DOMAIN      664    669       Poly-Leu.
FT   DOMAIN      808    811       Poly-Lys.
FT   DOMAIN      917    922       Poly-Ser.
FT   CARBOHYD     43     43       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     77     77       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     91     91       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    103    103       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    109    109       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    127    127       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    136    136       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    154    154       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    178    178       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    186    186       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    362    362       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    427    427       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    448    448       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    453    453       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    520    520       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    534    534       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    539    539       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    543    543       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    589    589       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    849    849       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC     40     66       Missing (in isoform 5).
FT                                 /FTId=VSP_009806.
FT   VARSPLIC     51     66       Missing (in isoform 4).
FT                                 /FTId=VSP_009807.
FT   VARSPLIC     64     66       Missing (in isoform 2).
FT                                 /FTId=VSP_009808.
FT   VARSPLIC     80     93       Missing (in isoform 3).
FT                                 /FTId=VSP_009809.
FT   CONFLICT    781    781       T -> K (in Ref. 2).
SQ   SEQUENCE   1009 AA;  110199 MW;  A53C67C5527A5B6C CRC64;

  Query Match             85.7%;  Score 54;  DB 1;  Length 1009;
  Best Local Similarity   80.0%;  Pred. No. 2.1;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||||:| |||
Db        770 CWINSNVVFY 779


RESULT 3
GP64_RAT
ID   GP64_RAT       STANDARD;      PRT;  1013 AA.
AC   Q8CJ11; Q8CJ06; Q8CJ07;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   G protein-coupled receptor 64 precursor (Epididymis-specific protein
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DE   6) (Re6 receptor).
GN   Name=Gpr64; Synonyms=Re6;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC   STRAIN=Lewis; TISSUE=Epididymis;
RX   MEDLINE=22307585; PubMed=12420295; DOI=10.1002/mrd.10220;
RA   Obermann H., Samalecos A., Osterhoff C., Schroeder B., Heller R.,
RA   Kirchhoff C.;
RT   "HE6, a two-subunit heptahelical receptor associated with apical
RT   membranes of efferent and epididymal duct epithelia.";
RL   Mol. Reprod. Dev. 64:13-26(2003).
CC   -!- FUNCTION: Could be involved in a signal transduction pathway
CC       controlling epidymal function and male fertility.
CC   -!- SUBUNIT: Forms a heterodimer, consisting of a large extracellular
CC       region linked to a seven-transmembrane moiety (Probable).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1; Synonyms=Long;
CC         IsoId=Q8CJ11-1; Sequence=Displayed;
CC       Name=2; Synonyms=d2;
CC         IsoId=Q8CJ11-2; Sequence=VSP_009810;
CC       Name=3; Synonyms=d1;
CC         IsoId=Q8CJ11-3; Sequence=VSP_009811;
CC   -!- TISSUE SPECIFICITY: Epididymys-specific expression. Both subunits
CC       were associated with apical membranes of efferent ductule and
CC       proximal epididymal duct epithelia.
CC   -!- PTM: Proteolytically cleaved into 2 subunits, an extracellular
CC       subunit and a seven-transmembrane subunit (Potential).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
CC       LN-TM7 subfamily.
CC   -!- SIMILARITY: Contains 1 GPS domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF538953; AAN33055.1; -.
DR   EMBL; AF538958; AAN33060.1; -.
DR   EMBL; AF538959; AAN33061.1; -.
DR   RGD; 628618; Gpr64.
DR   InterPro; IPR000832; GPCR_secretin.
DR   InterPro; IPR000203; PKD_cys_rich.
DR   Pfam; PF00002; 7tm_2; 1.
DR   Pfam; PF01825; GPS; 1.
DR   PRINTS; PR00249; GPCRSECRETIN.
DR   SMART; SM00303; GPS; 1.
DR   PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
DR   PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
DR   PROSITE; PS50221; GPS; 1.
KW   Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW   Signal; Transmembrane.
FT   SIGNAL       1     37       Potential.
FT   CHAIN       38   1013       G protein-coupled receptor 64.
FT   DOMAIN      38    623       Extracellular (Potential).
FT   TRANSMEM   624    644       1 (Potential).
FT   DOMAIN     645    663       Cytoplasmic (Potential).
FT   TRANSMEM   664    684       2 (Potential).
FT   DOMAIN     685    688       Extracellular (Potential).
FT   TRANSMEM   689    709       3 (Potential).
FT   DOMAIN     710    733       Cytoplasmic (Potential).
FT   TRANSMEM   734    754       4 (Potential).
FT   DOMAIN     755    785       Extracellular (Potential).
FT   TRANSMEM   786    806       5 (Potential).
FT   DOMAIN     807    830       Cytoplasmic (Potential).
FT   TRANSMEM   831    851       6 (Potential).
FT   DOMAIN     852    853       Extracellular (Potential).
FT   TRANSMEM   854    874       7 (Potential).
FT   DOMAIN     875   1013       Cytoplasmic (Potential).
FT   DOMAIN     563    614       GPS.
FT   DOMAIN     249    252       Poly-Ser.
FT   DOMAIN     668    673       Poly-Leu.
FT   DOMAIN     812    815       Poly-Lys.
FT   DOMAIN     921    926       Poly-Ser.
FT   CARBOHYD    44     44       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    78     78       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    92     92       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   128    128       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   137    137       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   155    155       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   179    179       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   187    187       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   366    366       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   431    431       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   452    452       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   457    457       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   524    524       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   538    538       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   543    543       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   547    547       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   593    593       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   777    777       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   853    853       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    40     67       Missing (in isoform 2).
FT                               /FTId=VSP_009810.
FT   VARSPLIC    52     67       Missing (in isoform 3).
FT                               /FTId=VSP_009811.
SQ   SEQUENCE   1013 AA;  110700 MW;  03C5467D84527216 CRC64;

  Query Match             77.8%;  Score 49;  DB 1;  Length 1013;
  Best Local Similarity   70.0%;  Pred. No. 14;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||||:: |||
Db        774 CWINSSVVFY 783


RESULT 4
Q20975
ID   Q20975      PRELIMINARY;      PRT;   578 AA.
AC   Q20975;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein F58B4.1a.
GN   Name=F58B4.1a; ORFNames=F58B4.1;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilkinson J.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z74038; CAA98497.2; -.
DR   PIR; T22904; T22904.
DR   HSSP; P07584; 1IAE.
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DR   WormBase; WBGene00003549; F58B4.1.
DR   WormPep; F58B4.1a; CE35881.
DR   GO; GO:0008533; F:astacin activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000859; CUB.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006026; Peptidase_M.
DR   InterPro; IPR001506; Peptidase_M12A.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR003582; ShKT.
DR   Pfam; PF01400; Astacin; 1.
DR   Pfam; PF01549; ShTK; 1.
DR   PRINTS; PR00480; ASTACIN.
DR   SMART; SM00254; ShKT; 1.
DR   SMART; SM00235; ZnMc; 1.
DR   PROSITE; PS01180; CUB; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   578 AA;  64678 MW;  2975A841FE70E5E2 CRC64;

  Query Match             74.6%;  Score 47;  DB 2;  Length 578;
  Best Local Similarity   70.0%;  Pred. No. 18;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||:|||  ||
Db        569 CWMNNNNNFY 578


RESULT 5
Q6CSG6
ID   Q6CSG6      PRELIMINARY;      PRT;   566 AA.
AC   Q6CSG6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Similar to sp|Q12001 Saccharomyces cerevisiae YOR002w ALG6
DE   glucosyltransferase.
GN   ORFNames=KLLA0D01221g;
OS   Kluyveromyces lactis NRRL Y-1140.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX   NCBI_TaxID=284590;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NRRL Y-1140;
RG   Genolevures;
RA   Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA   Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA   Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA   Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA   Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA   Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA   Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA   Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA   Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA   Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA   Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA   Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA   Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA   Wincker P., Souciet J.L.;
RT   "Genome evolution in yeasts.";
RL   Nature 430:35-44(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NRRL Y-1140;
RA   Genoscope;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR382124; CAH00219.1; -.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR004856; Alg6_Alg8.
DR   Pfam; PF03155; Alg6_Alg8; 1.
KW   Transferase.
SQ   SEQUENCE   566 AA;  65161 MW;  BEF7D2A4E2D6C074 CRC64;

  Query Match             69.8%;  Score 44;  DB 2;  Length 566;
  Best Local Similarity   77.8%;  Pred. No. 54;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVF 9
              |||||  |:|
Db        427 CWINNVALF 435


RESULT 6
G112_HUMAN
ID   G112_HUMAN     STANDARD;      PRT;  2799 AA.
AC   Q8IZF6; Q86SM6;
DT   25-OCT-2004 (Rel. 45, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   G-protein coupled receptor GPR112.
GN   Name=GPR112;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=12435584; DOI=10.1016/S0014-5793(02)03574-3;
RA   Fredriksson R., Lagerstroem M.C., Hoeglund P.J., Schioeth H.B.;
RT   "Novel human G protein-coupled receptors with long N-terminals
RT   containing GPS domains and Ser/Thr-rich regions.";
RL   FEBS Lett. 531:407-414(2002).
RN   [2]
RP   SEQUENCE OF 279-1549 FROM N.A.
RX   MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;
RA   Vassilatis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,
RA   Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
RA   Bergmann J.E., Gaitanaris G.A.;
RT   "The G protein-coupled receptor repertoires of human and mouse.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).
CC   -!- FUNCTION: Orphan receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
CC       LN-TM7 subfamily.
CC   -!- SIMILARITY: Contains 1 GPS domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AY140954; AAN46668.1; -.
DR   EMBL; AY255581; AAO85093.1; -.
DR   Genew; HGNC:18992; GPR112.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR000832; GPCR_secretin.
DR   InterPro; IPR000203; PKD_cys_rich.
DR   Pfam; PF00002; 7tm_2; 1.
DR   Pfam; PF01825; GPS; 1.
DR   PRINTS; PR00249; GPCRSECRETIN.
DR   SMART; SM00303; GPS; 1.
DR   PROSITE; PS50221; GPS; 1.
DR   PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
DR   PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
DR   PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; FALSE_NEG.
DR   PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN        1   2491       Extracellular (Potential).
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FT   TRANSMEM    2492    2512       1 (Potential).
FT   DOMAIN      2513    2527       Cytoplasmic (Potential).
FT   TRANSMEM    2528    2548       2 (Potential).
FT   DOMAIN      2549    2554       Extracellular (Potential).
FT   TRANSMEM    2555    2575       3 (Potential).
FT   DOMAIN      2576    2597       Cytoplasmic (Potential).
FT   TRANSMEM    2598    2618       4 (Potential).
FT   DOMAIN      2619    2640       Extracellular (Potential).
FT   TRANSMEM    2641    2661       5 (Potential).
FT   DOMAIN      2662    2690       Cytoplasmic (Potential).
FT   TRANSMEM    2691    2711       6 (Potential).
FT   DOMAIN      2712    2799       Extracellular (Potential).
FT   DOMAIN      2433    2483       GPS.
FT   DOMAIN       177    2209       Thr-rich.
FT   CARBOHYD     103     103       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     169     169       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     224     224       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     271     271       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     423     423       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     588     588       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     605     605       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     617     617       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     625     625       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     674     674       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     734     734       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     772     772       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     835     835       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     870     870       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     956     956       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     989     989       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1335    1335       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1369    1369       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1455    1455       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1504    1504       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1659    1659       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1991    1991       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    2029    2029       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    2218    2218       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    2256    2256       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    2305    2305       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    2322    2322       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    2354    2354       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    2391    2391       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    2450    2450       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    2462    2462       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   2799 AA;  300964 MW;  D3A31C9702A87B50 CRC64;

  Query Match             68.3%;  Score 43;  DB 1;  Length 2799;
  Best Local Similarity   50.0%;  Pred. No. 3.8e+02;
  Matches    5;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              ||| :::::||
Db       2634 CWIKDDSIFY 2643


RESULT 7
Q8IFE2
ID   Q8IFE2      PRELIMINARY;      PRT;   128 AA.
AC   Q8IFE2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein Tb927.1.1490.
GN   Name=Tb927.1.1490;
OS   Trypanosoma brucei.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX   NCBI_TaxID=5691;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TREU927;
RA   Hall N., Berriman M., Lennard N.J., Harris B.R., Hertz-Fowler C.,
RA   Bart-Delabesse E.N., Gerrare C.S., Atkin R.J., Barron A.J., Bowman S.,
RA   Bray-Allen S.P., Bringaud F., Clark L.N., Corton C.H., Cronin A.,
RA   Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper A.D.,
RA   Kay M.P., Leech V., Mayes R., Price C., Quail M.A., Rabbinowitch E.,
RA   Reitter C., Rutherford K., Sasse J., Sharp S., Shownkeen R.,
RA   Macleod A., Taylor S., Tweedie A., Turner C.M.R., Tait A., Gull K.,
RA   Barrell B., Melville S.E.;
RT   "The DNA sequence of chromosome I of an African trypanosome: gene
RT   content, chromosome organisation, recombination and polymorphism.";
RL   Nucleic Acids Res. 31:4864-4873(2003).
DR   EMBL; AL929604; CAD53076.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   128 AA;  15003 MW;  210093C812A19E37 CRC64;

  Query Match             66.7%;  Score 42;  DB 2;  Length 128;
  Best Local Similarity   55.6%;  Pred. No. 27;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVF 9
              || ||| ::
Db         81 CWFNNNNIY 89


RESULT 8
Q9LQW3
ID   Q9LQW3      PRELIMINARY;      PRT;   168 AA.
AC   Q9LQW3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   F10B6.7 (Hypothetical protein At1g14687).
GN   Name=At1g14687;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M.,
RA   Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
RA   Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S.,
RA   Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,
RA   Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA   Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA   Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA   Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA   Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA   Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA   Theologis A., Ecker J.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22088475; PubMed=12093376;
RA   Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA   Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT   "Full-length messenger RNA sequences greatly improve genome
RT   annotation.";
RL   Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA   Feldmann K.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA   Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA   Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
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RA   Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA   Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA   Theologis A.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA   Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA   Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA   Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA   Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA   Theologis A.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC006917; AAF79220.1; -.
DR   EMBL; AY086523; AAM63522.1; -.
DR   EMBL; BT003942; AAO41987.1; -.
DR   EMBL; BT005027; AAO50560.1; -.
DR   InterPro; IPR006455; Homeo_ZF_HD.
DR   InterPro; IPR006456; ZF_HD_N.
DR   Pfam; PF04770; ZF-HD_dimer; 1.
DR   TIGRFAMs; TIGR01565; homeo_ZF_HD; 1.
DR   TIGRFAMs; TIGR01566; ZF_HD_prot_N; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   168 AA;  19922 MW;  BFB868E8E0A32B94 CRC64;

  Query Match             66.7%;  Score 42;  DB 2;  Length 168;
  Best Local Similarity   66.7%;  Pred. No. 36;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 WINNNAVFY 10
              |:|||  ||
Db        159 WVNNNKKFY 167


RESULT 9
Q9EPE5
ID   Q9EPE5      PRELIMINARY;      PRT;   268 AA.
AC   Q9EPE5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lecithin cholesterol acyl transferase (Fragment).
GN   Name=lcat;
OS   Calomyscus mystax (Afghan mouse-like hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Calomyscinae;
OC   Calomyscus.
OX   NCBI_TaxID=109677;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20538273; PubMed=11083941; DOI=10.1006/mpev.2000.0849;
RA   Michaux J.R., Catzeflis F.M.;
RT   "The bushlike radiation of muroid rodents is exemplified by the
RT   molecular phylogeny of the LCAT nuclear gene.";
RL   Mol. Phylogenet. Evol. 17:280-293(2000).
DR   EMBL; AJ275538; CAC18113.1; -.
DR   EMBL; AJ275539; CAC18113.1; JOINED.
DR   EMBL; AJ275540; CAC18113.1; JOINED.
DR   EMBL; AJ275541; CAC18113.1; JOINED.
DR   EMBL; AJ275542; CAC18113.1; JOINED.
DR   GO; GO:0004607; F:phosphatidylcholine-sterol O-acyltransferas. . .; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006629; P:lipid metabolism; IEA.
DR   InterPro; IPR003386; LACT.
DR   InterPro; IPR008262; Lipase_AS.
DR   Pfam; PF02450; LACT; 1.
DR   PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW   Transferase.
FT   NON_TER       1      1
FT   NON_TER     268    268
SQ   SEQUENCE   268 AA;  30975 MW;  E733B8D375EA2533 CRC64;

  Query Match             66.7%;  Score 42;  DB 2;  Length 268;
  Best Local Similarity   60.0%;  Pred. No. 56;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:| :| |
Db         18 CWIDNTSVVY 27


RESULT 10
Q7RLD7
ID   Q7RLD7      PRELIMINARY;      PRT;   779 AA.
AC   Q7RLD7;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=PY02609;
OS   Plasmodium yoelii yoelii.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=73239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=17XNL;
RX   PubMed=12368865; DOI=10.1038/nature01099;
RA   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA   Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA   Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA   Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA   Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA   Florens L., Yates F.R. III, Raine J.D., Sinden R.E.; Harris M.A.,
RA   Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA   van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA   Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA   Carucci D.J.;
RT   "Genome sequence and comparative analysis of the model rodent malaria
RT   parasite Plasmodium yoelii yoelii.";
RL   Nature 419:512-519(2002).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABL01000716; EAA22076.1; -.
DR   InterPro; IPR001279; Blactmase-like.
DR   Pfam; PF00753; Lactamase_B; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   779 AA;  92558 MW;  BF20EE74D050B462 CRC64;

  Query Match             66.7%;  Score 42;  DB 2;  Length 779;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CWINNN 6
              ||||||
Db        433 CWINNN 438


RESULT 11
Q70UX2
ID   Q70UX2      PRELIMINARY;      PRT;   105 AA.
AC   Q70UX2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Lecithin cholesterol acyl transferase (Fragment).
GN   Name=lcat;
OS   Graphiurus platyops (rock dormouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Myoxidae; Graphiurinae;
OC   Graphiurus.
OX   NCBI_TaxID=221699;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Montgelard C., Matthee C.A., Robinson T.J.;
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RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ536378; CAD67534.1; -.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR003386; LACT.
DR   Pfam; PF02450; LACT; 1.
KW   Transferase.
FT   NON_TER       1      1
FT   NON_TER     105    105
SQ   SEQUENCE   105 AA;  11769 MW;  A52FDB70A7B2F5CC CRC64;

  Query Match           65.1%;  Score 41;  DB 2;  Length 105;
  Best Local Similarity   60.0%;  Pred. No. 33;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         17 CWIDNTRVIY 26


RESULT 12
Q70UX6
ID   Q70UX6      PRELIMINARY;      PRT;   125 AA.
AC   Q70UX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Lecithin cholesterol acyl transferase (Fragment).
GN   Name=lcat;
OS   Dryomys laniger (woolly dormouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Myoxidae; Leithiinae;
OC   Dryomys.
OX   NCBI_TaxID=221696;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Montgelard C., Matthee C.A., Robinson T.J.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ536374; CAD67532.1; -.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR003386; LACT.
DR   InterPro; IPR008262; Lipase_AS.
DR   Pfam; PF02450; LACT; 1.
DR   PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW   Transferase.
FT   NON_TER       1      1
FT   NON_TER     125    125
SQ   SEQUENCE   125 AA;  14467 MW;  1156855CEAB7B97D CRC64;

  Query Match           65.1%;  Score 41;  DB 2;  Length 125;
  Best Local Similarity   60.0%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         17 CWIDNTRVIY 26


RESULT 13
Q70UX1
ID   Q70UX1      PRELIMINARY;      PRT;   126 AA.
AC   Q70UX1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Lecithin cholesterol acyl transferase (Fragment).
GN   Name=lcat;
OS   Graphiurus ocularis (spectacled dormouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Myoxidae; Graphiurinae;
OC   Graphiurus.
OX   NCBI_TaxID=221698;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Montgelard C., Matthee C.A., Robinson T.J.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ536379; CAD67539.1; -.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR003386; LACT.
DR   InterPro; IPR008262; Lipase_AS.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF02450; LACT; 1.
DR   PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW   Transferase.
FT   NON_TER       1      1
FT   NON_TER     126    126
SQ   SEQUENCE   126 AA;  14461 MW;  DC978F5758D24EEB CRC64;

  Query Match           65.1%;  Score 41;  DB 2;  Length 126;
  Best Local Similarity   60.0%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         10 CWIDNTRVIY 19


RESULT 14
Q70UW9
ID   Q70UW9      PRELIMINARY;      PRT;   136 AA.
AC   Q70UW9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Lecithin cholesterol acyl transferase (Fragment).
GN   Name=lcat;
OS   Graphiurus lorraineus (Lorrain dormouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Myoxidae; Graphiurinae;
OC   Graphiurus.
OX   NCBI_TaxID=221682;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Montgelard C., Matthee C.A., Robinson T.J.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ536381; CAD67541.1; -.
DR   GO; GO:0004607; F:phosphatidylcholine-sterol O-acyltransferas. . .; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006629; P:lipid metabolism; IEA.
DR   InterPro; IPR003386; LACT.
DR   InterPro; IPR008262; Lipase_AS.
DR   Pfam; PF02450; LACT; 1.
DR   PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW   Transferase.
FT   NON_TER       1      1
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15779 MW;  C4477D97DC9B96B4 CRC64;

  Query Match           65.1%;  Score 41;  DB 2;  Length 136;
  Best Local Similarity   60.0%;  Pred. No. 42;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         17 CWIDNTRVIY 26


RESULT 15
Q70UX0
ID   Q70UX0      PRELIMINARY;      PRT;   136 AA.
AC   Q70UX0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Lecithin cholesterol acyl transferase (Fragment).
GN   Name=lcat;
OS   Graphiurus parvus (savanna dormouse).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Myoxidae; Graphiurinae;
OC   Graphiurus.
OX   NCBI_TaxID=221697;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Montgelard C., Matthee C.A., Robinson T.J.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ536380; CAD67540.1; -.
DR   GO; GO:0004607; F:phosphatidylcholine-sterol O-acyltransferas. . .; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006629; P:lipid metabolism; IEA.
DR   InterPro; IPR003386; LACT.
DR   InterPro; IPR008262; Lipase_AS.
DR   Pfam; PF02450; LACT; 1.
DR   PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW   Transferase.
FT   NON_TER       1      1
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15779 MW;  C4477D97DC9B96B4 CRC64;

  Query Match             65.1%;  Score 41;  DB 2;  Length 136;
  Best Local Similarity   60.0%;  Pred. No. 42;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CWINNNAVFY 10
              |||:|  | |
Db         17 CWIDNTRVIY 26


Search completed: October 20, 2005, 05:54:14
Job time : 59 secs
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